

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.

(ii) TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

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Street
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60603

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/688,356
(B) FILING DATE: 04-APR-1991

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 27866/30822

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(C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AARATGGGNA TGAARAARAA

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Met Gly Met Met Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACRTTCATYT CYTCYTCYTG CAT

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Met Gln Glu Glu Glu Met Asn Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 100..1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCAGAAA CTGTAGGAAT TCTGATGTGC TTCCGGTCAT GGAACAGTAA CAGATGAGCT	60
GCTTTGGGGA GAGCTGGAAC GCTCAGTCGG AGTATCATC ATG GGG TCT ACT GCT Met Gly Ser Thr Ala	114
1 5	
ACA GAA ACT GAA GAA CTG GAA AAC ACT ACT TTT AAG TAT CTC ATT GGA Thr Glu Thr Glu Leu Glu Asn Thr Thr Phe Lys Tyr Leu Ile Gly	162
10 15 20	
GAA CAG ACT GAA AAA ATG TGG CAA CGC CTG AAA GGA ATA CTA AGA TGC Glu Gln Thr Glu Lys Met Trp Gln Arg Leu Lys Gly Ile Leu Arg Cys	210
25 30 35	
TTA GTG AAG CAG CTG GAA AAA GGT GAT GTT AAC GTC ATC GAC TTA AAG Leu Val Lys Gln Leu Glu Lys Gly Asp Val Asn Val Ile Asp Leu Lys	258
40 45 50	
AAG AAT ATT GAA TAT GCA GCA TCT GTG TTG GAA GCA GTT TAT ATT GAT Lys Asn Ile Glu Tyr Ala Ala Ser Val Leu Glu Ala Val Tyr Ile Asp	306
55 60 65	
GAA ACA AGG AGA CTG CTG GAC ACC GAT GAG CTC AGT GAC ATT CAG Glu Thr Arg Arg Leu Leu Asp Thr Asp Asp Glu Leu Ser Asp Ile Gln	354
70 75 80 85	
TGG GAT TCC GTC CCA TCA GAA GTC CCG GAC TGG TTG GCT TCT ACC TTT Ser Asp Ser Val Pro Ser Glu Val Arg Asp Trp Leu Ala Ser Thr Phe	402
90 95 100	
ACA CGG AAA ATG CGG ATG ATG AAA AAG AAA TCT GAG GAA AAA CCA AGA Thr Arg Lys Met Gly Met Lys Lys Ser Glu Glu Lys Pro Arg	450
105 110 115	
TTT CGG AGC ATT GTG CAT GTT GTT CAA GCT GGA ATT TTT GTG GAA AGA Phe Arg Ser Ile Val His Val Val Gln Ala Gly Ile Phe Val Glu Arg	498
120 125 130	
ATG TAC AGA AAG TCC TAT CAC ATG GTT GGC TTG GCA TAT CCA GAG GCT Met Tyr Arg Lys Ser Tyr His Met Val Gly Leu Ala Tyr Pro Glu Ala	546
135 140 145	
GTC ATA GTA ACA TTA AAG GAT GTT GAT AAA TGG TCT TTT GAT GTA TTT Val Ile Val Thr Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe	594
150 155 160 165	
GCC TTG AAT GAA GCA AGT GGA GAA CAC AGT CTG AAG TTT ATG ATT TAT Ala Leu Asn Glu Ala Ser Gly Glu His Ser Leu Lys Phe Met Ile Tyr	642
-170 175 180	
GAA CTA TTC ACC AGA TAT GAT CTT ATC AAC CGT TTC AAG ATT CCT GTT Glu Leu Phe Thr Arg Tyr Asp Leu Ile Asn Arg Phe Lys Ile Pro Val	690
185 190 195	
TCT TGC CTA ATT GCC TTT GCA GAA GCT CTA GAA GTT GGT TAC AGC AAG Ser Cys Leu Ile Ala Phe Ala Glu Ala Leu Glu Val Gly Tyr Ser Lys	738
200 205 210	
TAC AAA AAT CCA TAC CAC AAT TTG ATT CAT GCA GCT GAT GTC ACT CAA Tyr Lys Asn Pro Tyr His Asn Leu Ile His Ala Ala Asp Val Thr Gln	786
215 220 225	
ACT GTG CAT TAC ATA ATG CTT CAT ACA GGT ATC ATG CAC TGG CTC ACT Thr Val His Tyr Ile Met Leu His Thr Gly Ile Met His Trp Leu Thr	834
230 235 240 245	

GAA CTG GAA ATT TTA GCA ATG GTC TTT GCC GCT GCC ATT CAT GAC TAT Glu Leu Glu Ile Leu Ala Met Val Phe Ala Ala Ala Ile His Asp Tyr 250 255 260	882
GAG CAT ACA GGG ACT ACA AAC AAT TTT CAC ATT CAG ACA AGG TCA GAT Glu His Thr Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp 265 270 275	930
GTT GCC ATT TTG TAT AAT GAT CGC TCT GTC CTT GAA AAT CAT CAT GTG Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Val 280 285 290	978
AGT GCA GCT TAT CGC CTT ATG CAA GAA GAA GAA ATG AAT GTC CTG ATA Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu Met Asn Val Leu Ile 295 300 305	1026
AAT TTA TCC AAA GAT GAC TGG AGG GAT CTT CGG AAC CTA GTG ATT GAA Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg Asn Leu Val Ile Glu 310 315 320 325	1074
ATG GTG TTG TCT ACA GAC ATG TCG GGT CAC TTC CAG CAA ATT AAA AAT Met Val Leu Ser Thr Asp Met Ser Gly His Phe Gln Gln Ile Lys Asn 330 335 340	1122
ATA AGA AAT AGT TTG CAG CAA CCT GAA GGG CTT GAC AAA GCC AAA ACC Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Leu Asp Lys Ala Lys Thr 345 350 355	1170
ATG TCC CTG ATT CTC CAT GCA GCA GAC ATC AGT CAC CCA GCC AAA TCC Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser His Pro Ala Lys Ser 360 365 370	1218
TGG AAG CTG CAC CAC CGA TGG ACC ATG GCC CTA ATG GAG GAG TTT TTC Trp Lys Leu His His Arg Trp Thr Met Ala Leu Met Glu Glu Phe Phe 375 380 385	1266
CTA CAG GGA GAT AAA GAA GCT GAA TTA GGG CTT CCA TTT TCC CCG CTT Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu 390 395 400 405	1314
TGC GAT CGG AAG TCA ACG ATG GTG GCC CAG TCC CAA ATA GGT TTC ATT Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser Gln Ile Gly Phe Ile 410 415 420	1362
GAT TTC ATA GTA GAA CCA ACA TTT TCT CTT CTG ACA GAC TCA ACA GAG Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu Thr Asp Ser Thr Glu 425 430 435	1410
AAA ATT ATT ATT CCT CTT ATA GAG GAA GAC TCG AAA ACC AAA ACT CCT Lys Ile Ile Ile Pro Leu Ile Glu Glu Asp Ser Lys Thr Lys Thr Pro 440 - 445 450	1458
TCC TAT GGA GCA AGC AGA CGA TCA AAT ATG AAA GGC ACC ACC AAT GAT Ser Tyr Gly Ala Ser Arg Arg Ser Asn Met Lys Gly Thr Thr Asn Asp 455 460 465	1506
GGA ACC TAC TCC CCC GAC TAC TCC CTT GCC AGC GTG GAC CTG AAG AGC Gly Thr Tyr Ser Pro Asp Tyr Ser Leu Ala Ser Val Asp Leu Lys Ser 470 475 480 485	1554
TTC AAA AAC AGC CTG GTG GAC ATC ATC CAG CAG AAC AAA GAG AGG TGG Phe Lys Asn Ser Leu Val Asp Ile Ile Gln Gln Asn Lys Glu Arg Trp 490 495 500	1602
AAA GAG TTA GCT GCT CAA GGT GAA CCT GAT CCC CAT AAG AAC TCA GAT Lys Glu Leu Ala Ala Gln Gly Glu Pro Asp Pro His Lys Asn S r Asp 505 510 515	1650

CTA GTA AAT GCT GAA GAA AAA CAT GCT GAA ACA CAT TCA TAGGTCTGAA	1699
Leu Val Asn Ala Glu Glu Lys His Ala Glu Thr His Ser	
520 525 530	
ACACCTGAAA GACGTCTTC ATTCTAAGGA TGGGAGGAAA CAAATTCAACA AGAAATCATG	1759
AAGACATATA AAAGCTACAT ATGCATAAAA AACTCTGAAT TCAGGTCCCC ATGGCTGTCA	1819
CAAATGAATG AACAGAACTC CCAACCCCGC CTTTTTAA TATAATGAAA GTGCCCTAGC	1879
ATGGTTGCAG CTGTCACAC TACAGTGT TACAGACGGT TTCTACTGAG CATCACAAATA	1939
AAGAGAATCT TGCATTACAA AAAAAAGAAA AAAATGTGGC TCGCTTTAA GATGAAGCAT	1999
TTCCCACTAT TTCTGAGTCA GTTGTAAAGAT TCTTAATCG ATACTAATAG TTTCACTAAT	2059
AGCCACTGTC AGTGTACAGC ACTGTGATGA AATCTTATAC TTAGTCCTTC AACAGTTCCA	2119
GAGTTGTGAC TGTGCTTAAT AGTTGCATA TGAATTCTGG ATAGAAATCA AATCACAAAC	2179
TGCATAGAAA TTTAAAAAC CAGCTCCATA TAAATTTT TTAAGATATT GTCTTGTATT	2239
GAAACTCCAA TACTTGGCC ACCTGATGCA AAGAGCTGAC TCATTTGAAA CC	2291

(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 530 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Met Gly Ser Thr Ala Thr Glu Thr Glu Glu Leu Glu Asn Thr Thr Phe	
1 5 10 15	
Lys Tyr Leu Ile Gly Glu Gln Thr Glu Lys Met Trp Gln Arg Leu Lys	
20 25 30	
Gly Ile Leu Arg Cys Leu Val Lys Gln Leu Glu Lys Gly Asp Val Asn	
35 40 45	
Val Ile Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala Ser Val Leu Glu	
50 55 60	
Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp Thr Asp Asp Glu	
65 70 75 80	
Leu Ser Asp Ile Gln Ser Asp Ser Val Pro Ser Glu Val Arg Asp Trp	
85 90 95	
Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Met Lys Lys Ser	
100 105 110	
Glu Glu Lys Pro Arg Phe Arg Ser Ile Val His Val Val Gln Ala Gly	
115 120 125	
Ile Phe Val Glu Arg Met Tyr Arg Lys Ser Tyr His Met Val Gly Leu	
130 135 140	
Ala Tyr Pro Glu Ala Val Ile Val Thr Leu Lys Asp Val Asp Lys Trp	
145 150 155 160	

Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly Glu His Ser Leu
165 170 175

Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp Leu Ile Asn Arg
180 185 190

Phe Lys Ile Pro Val Ser Cys Leu Ile Ala Phe Ala Glu Ala Leu Glu
195 200 205

Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn Leu Ile His Ala
210 215 220

Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu His Thr Gly Ile
225 230 235 240

Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met Val Phe Ala Ala
245 250 255

Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Asn Phe His Ile
260 265 270

Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu
275 280 285

Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu
290 295 300

Met Asn Val Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg
305 310 315 320

Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser Gly His Phe
325 330 335

Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Leu
340 345 350

Asp Lys Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser
355 360 365

His Pro Ala Lys Ser Trp Lys Leu His His Arg Trp Thr Met Ala Leu
370 375 380

Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
385 390 395 400

Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser
405 410 415

Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu
420 425 430

Thr Asp Ser Thr Glu Lys Ile Ile Pro Leu Ile Glu Glu Asp Ser
435 440 445

Lys Thr Lys Thr Pro Ser Tyr Gly Ala Ser Arg Arg Ser Asn Met Lys
450 455 460

Gly Thr Thr Asn Asp Gly Thr Tyr Ser Pro Asp Tyr Ser Leu Ala Ser
465 470 475 480

Val Asp Leu Lys Ser Phe Lys Asn Ser Leu Val Asp Ile Ile Gln Gln
485 490 495

Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Gly Glu Pro Asp Pro
500 505 510

His Lys Asn Ser Asp Leu Val Asn Ala Glu Glu Lys His Ala Glu Thr
515 520 525

His Ser
530

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Asp His Val Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGRAGRC AYGTHACNAT

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Cys Leu Val Lys Gln
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGCTTCACT AAGCATCTTA G

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGAAAGGC ACGTAACGAT CAGGAGGAAA CATCTCCAAA GACCCATCTT TAGACTAAGA
TGCTTAGTGA AGCAG

60

75

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAYGAYC ACGTAACGAT C

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGTATCTCA TTGGAGAAC A

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGGATGATC ACGTAACGAT CAGGAGGAAA CATCTCCAAA GACCCATCTT TAGA

54

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Asp His Val Thr Ile Arg Arg Lys His Leu Gln Arg Pro Ile
1 5 10 15

Phe Arg

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 136..1677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGCTGTCGA GAGAAAGAGG AAACTACTTT TGCCTTCTGG GCTCCTTGCA GGACAATAGA 60

TCAGGATAAG CTTCCACATT CTCTCCCTGG ATTTCTGGAG TGGTTTCCAG GAACAAGCTA 120

AACTTTCACC TTTAA ATG GAT GAC CAT GTC ACA ATC AGG AGG AAA CAT CTC 171
Met Asp Asp His Val Thr Ile Arg Arg Lys His Leu
- 1 5 10

CAA AGA CCC ATC TTT AGA CTA AGA TGC TTA GTG AAG CAG CTG GAA AAA 219
Gln Arg Pro Ile Phe Arg Leu Arg Cys Leu Val Lys Gln Leu Glu Lys
15 20 25

GGT GAT GTT AAC GTC ATC GAC TTA AAG AAG AAT ATT GAA TAT GCA GCA 267
Gly Asp Val Asn Val Ile Asp Leu Lys Asn Ile Glu Tyr Ala Ala
30 35 40

TCT GTG TTG GAA GCA GTT TAT ATT GAT GAA ACA AGG AGA CTG CTG GAC 315
Ser Val Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp
45 50 55 60

ACC GAT GAT GAG CTC AGT GAC ATT CAG TCG GAT TCC GTC CCA TCA GAA 363
Thr Asp Asp Glu Leu Ser Asp Ile Gln Ser Asp Ser Val Pro Ser Glu
65 70 75

GTC CGG GAC TGG TTG GCT TCT ACC TTT ACA CGG AAA ATG GGG ATG ATG Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Met	411
80 85 90	
AAA AAG AAA TCT GAG GAA AAA CCA AGA TTT CGG AGC ATT GTG CAT GTT Lys Lys Lys Ser Glu Glu Lys Pro Arg Phe Arg Ser Ile Val His Val	459
95 100 105	
GTT CAA GCT GGA ATT TTT GTG GAA AGA ATG TAC AGA AAG TCC TAT CAC Val Gln Ala Gly Ile Phe Val Glu Arg Met Tyr Arg Lys Ser Tyr His	507
110 115 120	
ATG GTT GGC TTG GCA TAT CCA GAG GCT GTC ATA GTA ACA TTA AAG GAT Met Val Gly Leu Ala Tyr Pro Glu Ala Val Ile Val Thr Leu Lys Asp	555
125 130 135 140	
GTT GAT AAA TGG TCT TTT GAT GTA TTT GCC TTG AAT GAA GCA AGT GGA Val Asp Lys Trp Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly	603
145 150 155	
GAA CAC AGT CTG AAG TTT ATG ATT TAT GAA CTA TTC ACC AGA TAT GAT Glu His Ser Leu Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp	651
160 165 170	
CTT ATC AAC CGT TTC AAG ATT CCT GTT TCT TGC CTA ATT GCC TTT GCA Leu Ile Asn Arg Phe Lys Ile Pro Val Ser Cys Leu Ile Ala Phe Ala	699
175 180 185	
GAA GCT CTA GAA GTT GGT TAC AGC AAG TAC AAA AAT CCA TAC CAC AAT Glu Ala Leu Glu Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn	747
190 195 200	
TTG ATT CAT GCA GCT GAT GTC ACT CAA ACT GTG CAT TAC ATA ATG CTT Leu Ile His Ala Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu	795
205 210 215 220	
CAT ACA GGT ATC ATG CAC TGG CTC ACT GAA CTG GAA ATT TTA GCA ATG His Thr Gly Ile Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met	843
225 230 235	
GTC TTT GCC GCT GCC ATT CAT GAC TAT GAG CAT ACA GGG ACT ACA AAC Val Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn	891
240 245 250	
AAT TTT CAC ATT CAG ACA AGG TCA GAT GTT GCC ATT TTG TAT AAT GAT Asn Phe His Ile Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp	939
255 260 265	
CGC TCT GTC CTT GAA AAT CAT CAT GTG AGT GCA GCT TAT CGC CTT ATG Arg Ser Val Leu Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met	987
270 275 280	
CAA GAA GAA GAA ATG AAT GTC CTG ATA AAT TTA TCC AAA GAT GAC TGG Gln Glu Glu Glu Met Asn Val Leu Ile Asn Leu Ser Lys Asp Asp Trp	1035
285 290 295 300	
AGG GAT CTT CCG AAC CTA GTG ATT GAA ATG GTG TTG TCT ACA GAC ATG Arg Asp Leu Arg Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met	1083
305 310 315	
TCG GGT CAC TTC CAG CAA ATT AAA AAT ATA AGA AAT AGT TTG CAG CAA Ser Gly His Phe Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln	1131
320 325 330	
CCT GAA GGG CTT GAC AAA GCC AAA ACC ATG TCC CTG ATT CTC CAT GCA Pro Glu Gly Leu Asp Lys Ala Lys Thr Met Ser Leu Ile Leu His Ala	1179
335 340 345	

GCA GAC ATC AGT CAC CCA GCC AAA TCC TGG AAG CTG CAC CAC CGA TGG Ala Asp Ile Ser His Pro Ala Lys Ser Trp Lys Leu His His Arg Trp 350 355 360	1227
ACC ATG GCC CTA ATG GAG GAG TTT TTC CTA CAG GGA GAT AAA GAA GCT Thr Met Ala Leu Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala 365 370 375 380	1275
GAA TTA GGG CTT CCA TTT TCC CCG CTT TGC GAT CGG AAG TCA ACG ATG Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met 385 390 395	1323
GTG GCC CAG TCC CAA ATA GGT TTC ATT GAT TTC ATA GTA GAA CCA ACA Val Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr 400 405 410	1371
TTT TCT CTT CTG ACA GAC TCA ACA GAG AAA ATT ATT ATT CCT CTT ATA Phe Ser Leu Leu Thr Asp Ser Thr Glu Lys Ile Ile Ile Pro Leu Ile 415 420 425	1419
GAG GAA GAC TCG AAA ACC AAA ACT CCT TCC TAT GGA GCA AGC AGA CGA Glu Glu Asp Ser Lys Thr Lys Thr Pro Ser Tyr Gly Ala Ser Arg Arg 430 435 440	1467
TCA AAT ATG AAA GGC ACC ACC AAT GAT GGA ACC TAC TCC CCC GAC TAC Ser Asn Met Lys Gly Thr Thr Asn Asp Gly Thr Tyr Ser Pro Asp Tyr 445 450 455 460	1515
TCC CTT GCC AGC GTG GAC CTG AAG AGC TTC AAA AAC AGC CTG GTG GAC Ser Leu Ala Ser Val Asp Leu Lys Ser Phe Lys Asn Ser Leu Val Asp 465 470 475	1563
ATC ATC CAG CAG AAC AAA GAG AGG TGG AAA GAG TTA GCT GCT CAA GGT Ile Ile Gln Gln Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Gly 480 485 490	1611
GAA CCT GAT CCC CAT AAG AAC TCA GAT CTA GTA AAT GCT GAA GAA AAA Glu Pro Asp Pro His Lys Asn Ser Asp Leu Val Asn Ala Glu Glu Lys 495 500 505	1659
CAT GCT GAA ACA CAT TCA TAGGTCTGAA ACACCTGAAA GACGTCTTC His Ala Glu Thr His Ser 510	1707
ATTCTAAGGA TGGGAGAGTG CTGTAACTAC AAAACTTCA AGCTTCTAAG TAAAAGGAAA	1767
GCAAAAACAA AATTACAGAA AAATATTTT GCAGCTCTGA GGCTATTAG ATTGTCCTTG	1827
TTGTTTAAA TACATGGAA CCAAGTGAGA AGAGGGCTG CTCAGAAGTT GTAGTCGAAG	1887
TCCTAAGACA ACAATGAAGC ATCAGAGCCC TGACTCTGTG ACCTGTGAA CTCTCGTTG	1947
TAACTCTCAA GCTGGGAAAC CACAGCGAAT CCTGTTCTG AAAGCAGTGA ACCAGCCTGC	2007
ATCCACCACT GTTATTGCAA AGCACGAAAG CATCACCCAC GTGGGGTCA TCACAATGCA	2067
AGTCACGCAA GACCTATGAC CAAGATGACA AGAACCTCCA GCCCTTGTG GAGACAGACA	2127
CTAGAACTGA GAGTGGGATT TGCCTTCTGG GGTGTTAAC CCATCAGGAT GTAACAAAAT	2187
ATATTACAGG TCAAGGGATA AGGGACAAGA AGTGTGTGTC TGTGTGTG TGTTGTATG	2247
TGCGCGCACT CAAAAATGTC TGTGAAATG GAAGCCCCACA CTCTTCTGCA CAGAGAGCAT	2307
TATTTGATGT GATTTATAAT TTTACTACAA ACAAACGAAC TGCAGCCATT GGAGACTGCT	2367
TCCTTGTCAAT GTTTGCCCTG AGCATGTGCA GAGCCTTGCC TTGTTCCAA ATTGAAGAAC	2427

TACCTTTATT TGTTATTAGC TGCCAAGAAA GGTCAAGCCC AAGTAGGTGT TGTCACTTTC	2487
ACCGTACAAA CTCTTCAATG ATTGTTAGAC TAAAGGAATT TGTTTTGTG AAAGGTAGAA	2547
ATTAGATGGA AAAGATCAAG AGTAGTCATC AATTAAAGAA GAAAGTGAAG GTGGATATGT	2607
CCATCCTAAT GAGTTTCTG TTGCACCTGC TTCTCCCTG CGACAGCAA	2656

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 514 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Asp Asp His Val Thr Ile Arg Arg Lys His Leu Gln Arg Pro Ile	
1 5 10 15	
Phe Arg Leu Arg Cys Leu Val Lys Gln Leu Glu Lys Gly Asp Val Asn	
20 25 30	
Val Ile Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala Ser Val Leu Glu	
35 40 45	
Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp Thr Asp Asp Glu	
50 55 60	
Leu Ser Asp Ile Gln Ser Asp Ser Val Pro Ser Glu Val Arg Asp Trp	
65 70 75 80	
Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Met Lys Lys Ser	
85 90 95	
Glu Glu Lys Pro Arg Phe Arg Ser Ile Val His Val Val Gln Ala Gly	
100 105 110	
Ile Phe Val Glu Arg Met Tyr Arg Lys Ser Tyr His Met Val Gly Leu	
115 120 125	
Ala Tyr Pro Glu Ala Val Ile Val Thr Leu Lys Asp Val Asp Lys Trp	
130 135 140	
Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly Glu His Ser Leu	
145 150 155 160	
Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp Leu Ile Asn Arg	
165 170 175	
Phe Lys Ile Pro Val Ser Cys Leu Ile Ala Phe Ala Glu Ala Leu Glu	
180 185 190	
Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn Leu Ile His Ala	
195 200 205	
Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu His Thr Gly Ile	
210 215 220	
Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met Val Phe Ala Ala	
225 230 235 240	
Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Asn Phe His Ile	
245 250 255	

Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu
260 265 270

Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu
275 280 285

Met Asn Val Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg
290 295 300

Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser Gly His Phe
305 310 315 320

Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Leu
325 330 335

Asp Lys Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser
340 345 350

His Pro Ala Lys Ser Trp Lys Leu His His Arg Trp Thr Met Ala Leu
355 360 365

Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
370 375 380

Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser
385 390 395 400

Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu
405 410 415

Thr Asp Ser Thr Glu Lys Ile Ile Pro Leu Ile Glu Glu Asp Ser
420 425 430

Lys Thr Lys Thr Pro Ser Tyr Gly Ala Ser Arg Arg Ser Asn Met Lys
435 440 445

Gly Thr Thr Asn Asp Gly Thr Tyr Ser Pro Asp Tyr Ser Leu Ala Ser
450 455 460

Val Asp Leu Lys Ser Phe Lys Asn Ser Leu Val Asp Ile Ile Gln Gln
465 470 475 480

Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Gly Glu Pro Asp Pro
485 490 495

His Lys Asn Ser Asp Leu Val Asn Ala Glu Glu Lys His Ala Glu Thr
500 505 510

His Ser

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATHCAYGAYT AYGARCAYAC NGG

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile His Asp Tyr Glu His Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCYTTRTCNC CYTGNCGRAA RAAAYTCYTCC AT

32

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATT CAT GAT TAT AAC ACA CGG GGC ACT ACC AAC AGC TTC CAC ATC CAG Ile His Asp Tyr Asn Thr Arg Gly Thr Thr Asn Ser Phe His Ile Gln	48
1 5 10 15	
ACC AAA TCG GAA TGC GCC ATC CTG TAC AAC GAC CGC TCA GTG CTG GAG Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu	96
20 25 30	
AAT CAC CAC ATC AGC TCG GTT TTC CGA ATG ATG CAG GAC GAC GAC ATG Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp Asp Asp Met	144
35 40 45	
AAC ATC TTC ATC AAC CTC ACC AAG GAT GAG TTT GTA GAG CTG CCG GCT Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg Ala	192
50 55 60	
CTG GTC ATT GAG ATG GTG TTG GCC ACA GAC ATG TCC TGC CAT TTC CAG Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe Gln	240
65 70 75 80	
CAA GTG AAG TCC ATG AAG ACA GCC TTG CAG CAG CTG GAG AGG ATT GAC Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile Asp	288
85 90 95	
AAG TCC AAG GCC CTC TCT CTG CTG CTT CAT GCT GCT GAC ATC AGC CAC Lys Ser Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser His	336
100 105 110	
CCC ACC AAG CAG TGG TCG GTT CAC AGC CGC TGG ACC AAG GCC CTC ATG Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys Ala Leu Met	384
115 120 125	
GAG GAG TTC TTC CGA CAA GGG GAC AAA G Glu Glu Phe Phe Arg Gln Gly Asp Lys	412
130 135	

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile His Asp Tyr Asn Thr Arg Gly Thr Thr Asn Ser Phe His Ile Gln	
1 5 10 15	
Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu	
20 25 30	
Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp Asp Asp Met	
35 40 45	
Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg Ala	
50 55 60	
Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe Gln	
65 70 75 80	
Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile Asp	
85 90 95	

Lys Ser Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser His
100 105 110

Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys Ala Leu Met
115 120 125

Glu Glu Phe Phe Arg Gln Gly Asp Lys
130 135

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AARAARAAYY TNGARTAYAC NGC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys Lys Asn Leu Glu Tyr Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1844 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 114..1715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTGGGCAG CGGGAAAGGA GGAGCCGCAG GAACTGCAGC TCTGCCAGCT TGGGCCGAGC

60

TTTAGAGACC CCCGCCCTGG CTGGTCCCTG CCAGCCGCAG ACGGAGGCTG AGC ATG

116

Met
1

GAG CTG TCC CCC CGC AGC CCT CCC GAG ATG CTA GAG TCG GAC TGC CCT Glu Leu Ser Pro Arg Ser Pro Pro Glu Met Leu Glu Ser Asp Cys Pro 5 10 15	164
TCA CCC CTG GAG CTG AAG TCA GCC CCC AGC AAG AAG ATG TGG ATT AAG Ser Pro Leu Glu Leu Lys Ser Ala Pro Ser Lys Lys Met Trp Ile Lys 20 25 30	212
CTC CGG TCT CTG CTG CGC TAC ATG GTG AAG CAG TTG GAG AAC GGG GAG Leu Arg Ser Leu Leu Arg Tyr Met Val Lys Gln Leu Glu Asn Gly Glu 35 40 45	260
GTA AAC ATT GAG GAG CTG AAG AAA AAC CTG GAG TAC ACA GCT TCT CTG Val Asn Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala Ser Leu 50 55 60 65	308
CTG GAG GCC GTC TAT ATA GAT GAG ACT CGG CAA ATC CTG GAC ACG GAG Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp Thr Glu 70 75 80	356
GAT GAG CTG CAG GAG CTG CGG TCT GAT GCG GTG CCT TCA GAG GTG CGG Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu Val Arg 85 90 95	404
GAC TGG CTG GCC TCC ACC TTC ACC CAG CAG ACC CGG GCC AAA GGC CCG Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Thr Arg Ala Lys Gly Pro 100 105 110	452
AGC GAA GAG AAG CCC AAG TTC CCG AGC ATC GTG CAC GCG GTG CAG GCT Ser Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala 115 120 125	500
GGC ATC TTT GTG GAG CGG ATG TTC CCG AGA ACG TAC ACC TCT GTG GGC Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr Ser Val Gly 130 135 140 145	548
CCC ACC TAC TCC ACT GCC GTC CTC AAC TGT CTC AAG AAC GTG GAC CTT Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn Val Asp Leu 150 155 160	596
TGG TGC TTT GAT GTC TTT TCC TTG AAC CGG GCA GCA GAT GAC CAC GCC Trp Cys Phe Asp Val Phe Ser Leu Asn Arg Ala Ala Asp Asp His Ala 165 170 175	644
CTG AGG ACC ATC GTT TTT GAG CTG CTG ACT CGG CAC AAC CTC ATC AGC Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn Leu Ile Ser 180 185 190	692
CGC TTT AAG ATT CCC ACT GTG TTT TTG ATG ACT TTC CTG GAT GCC TTG Arg Phe Lys Ile Pro Thr Val Phe Leu Met Thr Phe Leu Asp Ala Leu 195 200 205	740
GAG ACA GGC TAC GGA AAG TAC AAG AAC CCT TAC CAC AAC CAG ATC CAC Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn Gln Ile His 210 215 220 225	788
GCA GCT GAC GTC ACC CAG ACG GTC CAC TGC TTC TTG CTC CGC ACA GGG Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu Arg Thr Gly 230 235 240	836
ATG GTG CAC TGC TCG TCG GAG ATT GAG GTC CTG GCC ATC ATC TTT GCT Met Val His Cys Leu Ser Glu Ile Glu Val Leu Ala Ile Ile Phe Ala 245 250 255	884
GCA GCG ATC CAC GAC TAT GAG CAC ACT GGC ACT ACC AAC AGC TTC CAC Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Ser Phe His 260 265 270	932

ATC CAG ACC AAA TCG GAA TGC GCC ATC CTG TAC AAC GAC CGC TCA GTG Ile Gln Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val 275 280 285	980
CTG GAG AAT CAC CAC ATC AGC TCG GTT TTC CGA ATG ATG CAG GAC GAC Leu Glu Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp Asp 290 295 300 305	1028
GAG ATG AAC ATC TTC ATC AAC CTC ACC AAG GAT GAG TTT GTA GAG CTG Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu 310 315 320	1076
CGG GCT CTG GTC ATT GAG ATG GTG TTG GCC ACA GAC ATG TCC TGC CAT Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His 325 330 335	1124
TTC CAG CAA GTG AAG TCC ATG AAG ACA GCC TTG CAG CAG CTG GAG AGG Phe Gln Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu Arg 340 345 350	1172
ATT GAC AAG TCC AAG GCC CTC TCT CTG CTG CTT CAT GCT GCT GAC ATC Ile Asp Lys Ser Lys Ala Leu Ser Leu Leu His Ala Ala Asp Ile 355 360 365	1220
AGC CAC CCC ACC AAG CAG TGG TCG GTT CAC AGC CGC TGG ACC AAG GCC Ser His Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys Ala 370 375 380 385	1268
CTC ATG GAG GAA TTC TTC CGC CAG GGT GAC AAG GAG GCT GAG CTG GGC Leu Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala Glu Leu Gly 390 395 400	1316
CTG CCC TTT TCT CCG CTC TGT GAC CGC ACT TCC ACC CTC GTG GCG CAG Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu Val Ala Gln 405 410 415	1364
TCC CAG ATT GGT TTC ATC GAC TTC ATT GTG GAG CCC ACG TTC TCT GTG Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Val 420 425 430	1412
CTC ACC GAT GTG GCT GAG AAG AGT GTC CAG CCC ACC GGG GAC GAC GAC Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Thr Gly Asp Asp Asp 435 440 445	1460
TCG AAG TCT AAA AAC CAG CCC AGC TTC CAG TGG CGC CAG CCT TCT CTG Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln Pro Ser Leu 450 455 460 465	1508
GAT GTA GAA GTG GGA GAC CCC AAC CCT GAC GTG GTC AGC TTC CGC TCC Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser Phe Arg Ser 470 475 480	1556
ACC TGG ACC AAA TAC ATT CAG GAG AAC AAG CAG AAA TGG AAG GAA CGG Thr Trp Thr Lys Tyr Ile Gln Glu Asn Lys Gln Lys Trp Lys Glu Arg 485 490 495	1604
GCG GCG AGC GGC ATC ACC AAC CAG ATG TCC ATT GAC GAA CTG TCC CCT Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu Leu Ser Pro 500 505 510	1652
TGT GAG GAA GAG GCC CCA GCC TCC CCT GCC GAA GAC GAG CAC AAC CAG Cys Glu Glu Glu Ala Pro Ala Ser Pro Ala Glu Asp Glu His Asn Gln 515 520 525	1700
AAC GGG AAT CTG GAC TAGCGGGGCC TGGCCAGGTC CTCACTGAGT CCTGAGTGTT Asn Gly Asn Leu Asp 530	1755

CGATGTCATC AGCACCATCC ATCGGGACTG GCTCCCCAT CTGCTCCGAG GGCGAATGGA	1815
TGTCAAGGAA CAGAAAACCC ACCCGAAGA	1844

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Leu Ser Pro Arg Ser Pro Pro Glu Met Leu Glu Ser Asp Cys	
1 5 10 15	
Pro Ser Pro Leu Glu Leu Lys Ser Ala Pro Ser Lys Lys Met Trp Ile	
20 25 30	
Lys Leu Arg Ser Leu Leu Arg Tyr Met Val Lys Gln Leu Glu Asn Gly	
35 40 45	
Glu Val Asn Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala Ser	
50 55 60	
Leu Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp Thr	
65 70 75 80	
Glu Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu Val	
85 90 95	
Arg Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Thr Arg Ala Lys Gly	
100 105 110	
Pro Ser Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln	
115 120 125	
Ala Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr Ser Val	
130 135 140	
Gly Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn Val Asp	
145 150 155 160	
Leu Trp Cys Phe Asp Val Phe Ser Leu Asn Arg Ala Ala Asp Asp His	
165 170 175	
Ala Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn Leu Ile	
180 185 190	
Ser Arg Phe Lys Ile Pro Thr Val Phe Leu Met Thr Phe Leu Asp Ala	
195 200 205	
Leu Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn Gln Ile	
210 215 220	
His Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu Arg Thr	
225 230 235 240	
Gly Met Val His Cys Leu Ser Glu Ile Glu Val Leu Ala Ile Ile Phe	
245 250 255	
Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Ser Phe	
260 265 270	

His Ile Gln Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser
275 280 285

Val Leu Glu Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp
290 295 300

Asp Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu
305 310 315 320

Leu Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys
325 330 335

His Phe Gln Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu
340 345 350

Arg Ile Asp Lys Ser Lys Ala Leu Ser Leu Leu His Ala Ala Asp
355 360 365

Ile Ser His Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys
370 375 380

Ala Leu Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala Glu Leu
385 390 395 400

Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu Val Ala
405 410 415

Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser
420 425 430

Val Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Thr Gly Asp Asp
435 440 445

Asp Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln Pro Ser
450 455 460

Leu Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser Phe Arg
465 470 475 480

Ser Thr Trp Thr Lys Tyr Ile Gln Glu Asn Lys Gln Lys Trp Lys Glu
485 490 495

Arg Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu Leu Ser
500 505 510

Pro Cys Glu Glu Glu Ala Pro Ala Ser Pro Ala Glu Asp Glu His Asn
515 520 525

Gln Asn Gly Asn Leu Asp
530

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Leu Glu Asn Gly Glu Val Asn Ile Glu Glu Leu Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gln Leu Ile Pro Gly Arg Val Asn Ile Ile Ser Leu Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys Asp Glu Thr Ala Ile Leu Tyr Asn Asp Arg Thr Val Leu Glu Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGATCCGGAT CCCGCAGACG GAGGCTGAGC ATGG

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCGGAT CCAGGACCTG GCCAGGCCCG GC

32

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Met Met Met Tyr His Met Lys
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Tyr His Asn Trp Met His Ala Phe
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCATRTGRT ACATCATCAT YTC

23

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AANGCRTGCA TCCARTTRTG RTA

23

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 148..2910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGGCGCAGCG	GCCGGGCCGG	CGGGCGGGCG	GGCGGCTGCG	AGCATGGTCC	TGGTGTGCA	60
CCACATCCTC	ATCGCTGTTG	TCCAATTCTT	CAGGCAGGGC	CAGCAGGTCT	TCCTCAAGCC	120
GGACGAGCGG	CCGCGGCCGC	CGCAGCC	ATG CGC CGA CAG CCT GCA GCC AGC			171
			Met Arg Arg Gln Pro Ala Ala Ser			
			1	5		
CGG GAC CTC TTT GCA CAG GAG CCA GTG CCC CCA GGG AGT GGA GAC GGC						219
Arg Asp Leu Phe Ala Gln Glu Pro Val Pro Pro Gly Ser Gly Asp Gly						
10	15	20				
GCA TTG CAG GAT GCT TTG CTG AGC CTG GGC TCC GTC ATC GAC GTT GCA						267
Ala Leu Gln Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Val Ala						
25	30	35	40			
GGC TTG CAA CAG GCT GTC AAG GAG GCC CTG TCG GCT GTG CTT CCC AAA						315
Gly Leu Gln Gln Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Lys						
45	50	55				
GTG GAG ACG GTC TAC ACC TAC CTG CTG GAT GGG GAA TCC CGG CTG GTG						363
Val Glu Thr Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Arg Leu Val						
60	65	70				
TGT GAG GAG CCC CCC CAC GAG CTG CCC CAG GAG GGG AAA GTG CGA GAG						411
Cys Glu Glu Pro Pro His Glu Leu Pro Gln Glu Gly Lys Val Arg Glu						
75	80	85				
GCT GTG ATC TCC CGG AAG CGG CTG GGC TGC AAT GGA CTG GGC CCC TCA						459
Ala Val Ile Ser Arg Lys Arg Leu Gly Cys Asn Gly Leu Gly Pr S r						
90	95	100				

GAC CTG CCT GGG AAG CCC TTG GCA AGG CTG GTG GCT CCA CTG GCT CCT Asp Leu Pro Gly Lys Pro Leu Ala Arg Leu Val Ala Pro Leu Ala Pro 105 110 115 120	507
GAC ACC CAA GTG CTG GTC ATA CCG CTG GTG GAC AAG GAG GCC GGG GCT Asp Thr Gln Val Leu Val Ile Pro Leu Val Asp Lys Glu Ala Gly Ala 125 130 135	555
GTG GCA GCT GTC ATC TTG GTG CAC TGT GGT CAG CTG AGT GAC AAT GAG Val Ala Ala Val Ile Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu 140 145 150	603
GAG TGG AGC CTG CAA GCT GTG GAG AAG CAT ACC CTG GTG GCC CTG AAA Glu Trp Ser Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Lys 155 160 165	651
AGG GTG CAG GCC TTG CAG CAG CGC GAG TCC AGC GTG GCC CCG GAA GCG Arg Val Gln Ala Leu Gln Gln Arg Glu Ser Ser Val Ala Pro Glu Ala 170 175 180	699
ACC CAG AAT CCT CCG GAG GAG GCA GCG GGA GAC CAG AAG GGT GGG GTC Thr Gln Asn Pro Pro Glu Ala Ala Gly Asp Gln Lys Gly Gly Val 185 190 195 200	747
GCA TAC ACA AAC CAA GAC CGA AAG ATC CTG CAG CTT TGC GGG GAG CTC Ala Tyr Thr Asn Gln Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu 205 210 215	795
TAC GAC CTG GAT GCA TCT TCC CTG CAG CTC AAA GTC CTC CAA TAT CTG Tyr Asp Leu Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu 220 225 230	843
CAA CAG GAG ACC CAG GCA TCC CGC TGC TGC CTG CTG CTG GTA TCC GAG Gln Gln Glu Thr Gln Ala Ser Arg Cys Cys Leu Leu Leu Val Ser Glu 235 240 245	891
GAC AAT CTT CAG CTC TCC TGC AAG GTC ATT GGA GAT AAA GTA CTG GAG Asp Asn Leu Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Glu 250 255 260	939
GAA GAG ATC AGC TTT CCG TTG ACC ACA GGA CGC CTG GGC CAA GTG GTG Glu Glu Ile Ser Phe Pro Leu Thr Thr Gly Arg Leu Gly Gln Val Val 265 270 275 280	987
GAA GAC AAG AAG TCT ATC CAG CTG AAA GAT CTC ACC TCC GAG GAT ATG Gly Asp Lys Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Met 285 290 295	1035
CAA CAG CTG CAA AGC ATG TTG GGC TGT GAG GTG CAG GCC ATG CTC TGT Gln Gln Leu Gln Ser Met Leu Gly Cys Glu Val Gln Ala Met Leu Cys 300 305 310	1083
GTC CCT GTC ATC AGC CGG GCC ACT GAC CAG GTC GTG GCC CTG GCC TGT Val Pro Val Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys 315 320 325	1131
GCC TTC AAC AAG CTC GGA GGA GAC TTG TTC ACA GAC CAG GAC GAG CAC Ala Phe Asn Lys Leu Gly Gly Asp Leu Phe Thr Asp Gln Asp Glu His 330 335 340	1179
GTG ATC CAG CAC TGC TTC CAC TAC ACC AGC ACA GTG CTC ACC AGC ACC Val Ile Gln His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr 345 350 355 360	1227
CTG GCC TTC CAG AAG GAG CAG AAG CTC AAG TGT GAG TGC CAG GCT CTT Leu Ala Phe Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu 365 370 375	1275

CTC CAA GTG GCG AAG AAC CTC TTC ACT CAT CTG GAT GAC GTC TCC GTG Leu Gln Val Ala Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val 380 385 390	1323
CTG CTC CAG GAG ATC ATC ACA GAG GCC AGG AAC CTC AGC AAT GCT GAG Leu Leu Gln Glu Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu 395 400 405	1371
ATC TGC TCT GTG TTC CTG CTG GAT CAG AAC GAG CTG GTG GCC AAG GTG Ile Cys Ser Val Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val 410 415 420	1419
TTC GAT GGG GGT GTG GTG GAA GAT GAG AGC TAT GAG ATC CGC ATT CCC Phe Asp Gly Gly Val Val Glu Asp Glu Ser Tyr Glu Ile Arg Ile Pro 425 430 435 440	1467
GCT GAC CAG GGC ATC GCG GGT CAT GTG GCG ACC ACC GGC CAG ATC CTA Ala Asp Gln Gly Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu 445 450 455	1515
AAC ATC CCA GAT GCT TAC GCA CAT CCG CTT TTC TAC CGA GGC GTG GAC Asn Ile Pro Asp Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp 460 465 470	1563
GAC AGC ACC GGC TTC CGG ACG CGC AAC ATC CTC TGC TTC CCC ATC AAG Asp Ser Thr Gly Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys 475 480 485	1611
AAC GAG AAC CAG GAG GTC ATC GGT GTG GCC GAG CTG GTG AAC AAG ATC Asn Glu Asn Gln Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile 490 495 500	1659
AAT GGA CCA TGG TTC AGC AAG TTT GAT GAA GAC CTG GCT ACA GCC TTC Asn Gly Pro Trp Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe 505 510 515 520	1707
TCC ATC TAC TGT GGC ATC AGC ATT GCC CAT TCC CTC CTA TAC AAG AAA Ser Ile Tyr Cys Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys 525 530 535	1755
GTG AAT GAG GCG CAG TAT CGC AGC CAC CTT GCC AAT GAG ATG ATG ATG Val Asn Glu Ala Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met 540 545 550	1803
TAC CAC ATG AAG GTC TCT GAT GAC GAG TAC ACC AAA CTT CTC CAT GAC Tyr His Met Lys Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp 555 560 565	1851
GGG ATC CAG CCT GTG GCT GCC ATC GAC TCC AAC TTT GCC AGT TTC ACA Gly Ile Gln Pro Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr 570 575 580	1899
TAC ACT CCT CGC TCT CTG CCC GAG GAT GAC ACT TCC ATG GCC ATC CTG Tyr Thr Pro Arg Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu 585 590 595 600	1947
AGC ATG CTG CAG GAC ATG AAT TTC ATC AAT AAC TAC AAA ATT GAC TGC Ser Met Leu Gln Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys 605 610 615	1995
CCG ACA CTG GCC CGG TTC TGT TTG ATG GTG AAG AAG GGC TAC CGG GAT Pro Thr Leu Ala Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp 620 625 630	2043
CCC CCC TAC CAC AAC TGG ATG CAC GCC TTT TCT GTC TCC CAC TTC TGC Pro Pro Tyr His Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys 635 640 645	2091

TAC CTG CTC TAC AAG AAC CTG GAG CTC ACC AAC TAC CTC GAG GAC ATG Tyr Leu Leu Tyr Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Met 650 655 660	2139
GAG ATC TTT GCC TTG TTT ATT TCC TGC ATG TGT CAC GAC CTG GAC CAC Glu Ile Phe Ala Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His 665 670 675 680	2187
AGA GGC ACA AAC AAC TCC TTC CAG GTG GCC TCG AAA TCT GTG CTG GCC Arg Gly Thr Asn Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala 685 690 695	2235
GCG CTC TAC AGC TCG GAA GGC TCT GTC ATG GAG AGG CAC CAC TTC GCT Ala Leu Tyr Ser Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala 700 705 710	2283
CAG GCC ATT GCC ATC CTC AAC ACC CAC GGC TGC AAC ATC TTT GAC CAC Gln Ala Ile Ala Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His 715 720 725	2331
TTC TCC CGG AAG GAT TAT CAG CGC ATG TTG GAC CTG ATG CGG GAC ATC Phe Ser Arg Lys Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile 730 735 740	2379
ATC TTG GCC ACA GAT CTG GCC CAC CAC CTC CGC ATC TTC AAG GAC CTC Ile Leu Ala Thr Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu 745 750 755 760	2427
CAA AAG ATG GCC GAA GTG GGC TAT GAT CGA ACC AAC AAG CAG CAC CAC Gln Lys Met Ala Glu Val Gly Tyr Asp Arg Thr Asn Lys Gln His His 765 770 775	2475
AGC CTC CTT CTC TGC CTC CTT ATG ACC TCC TGT GAC CTC TCT GAC CAG Ser Leu Leu Leu Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln 780 785 790	2523
ACC AAG GGC TGG AAG ACC ACG AGG AAG ATC GCG GAG CTG ATC TAC AAA Thr Lys Gly Trp Lys Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys 795 800 805	2571
GAG TTC TCC CAG GGA GAC TTG GAG AAG GCC ATG GGC AAC AGG CCG Glu Phe Ser Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro 810 815 820	2619
ATG GAG ATG ATG GAC CGT GAG AAG GCC TAC ATC CCC GAG CTG CAG ATC Met Glu Met Met Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile 825 830 835 840	2667
AGC TTC ATG GAG CAC ATC GCA ATG CCC ATC TAC AAG CTG CTG CAA GAC Ser Phe Met Glu His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp 845 850 855	2715
CTG TTC CCC AAG GCG GCC GAG TTG TAC GAA CGC GTG GCC TCT AAT CGT Leu Phe Pro Lys Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg 860 865 870	2763
GAG CAC TGG ACC AAG GTG TCA CAC AAG TTC ACC ATC CGA GGC CTC CCG Glu His Trp Thr Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro 875 880 885	2811
AGC AAC AAC TCG TTG GAC TTC CTG GAC GAG GAG TAT GAG GTG CCT GAC Ser Asn Asn Ser Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp 890 895 900	2859
CTG GAT GGC GCT AGG GCT CCC ATC AAT GGC TGT TGC AGC CTT GAT GCT Leu Asp Gly Ala Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala 905 910 915 920	2907

GAG TGAGTCCCTC CTGGGACCCC TCCCTGTCCA GGCCTCCTCC CACAAGCCTC Glu	2960
CACGGGCCTG GCCGCACGCC CTGGGACCAAG AGCCAAGGGT CCTGGATTCT AGGCCAGGAC TTCCCATGTG ACCCGGGCGA GGTCTGACCT TCCCGGGCCT CAGCTTCTT GTCTGTATAA TGGAAAGACTT CAGCCTCACT GAGACTTTGT CACTTGTCTT CTGAGAGCAC AGGGGTAACC AATGAGCAGT GGACCTGCT CTGCACCTCT GACCGCATCT TGGCAAGTCC CCACCCCTCCA GGCCACTCCT TCTCTGAGGC AGCCGGATGG TTTCTCTGG GCCCCATTCC TGCCCTACCA GACCTGTGCC CTTTCTGTG GGGGCACCTC CACTGGCTCC CAGGATCCTC AGGCAAGAAC ATGAGACATC TGAGTGGCA AAGGGTGGGT CTTAGAGACA GTTATCAGCC TGGCTGGAGG ACTAGAAGTA GCCATGGAC CACCTGTGGC CCAGAGGACT GCCTTGATAC TTATGGTGGG GAATGGGACC TGGGGATATA AGGGTCCCAG GAGGACACTG CCAGGGGCC AGTGCAGTGC TCTGGGAGA GGGGCTCAG GAAGAGAGGA GGATAAGAAC AGTGAGAAGG AAGGATCCCT GGGTTGGGAG GCAGGCCAG CATGGTCAG CCATGCTTCC TCCTGGCTGT GTGACCCCTGG GCAAGTCCCT TCCCCTCTCT CGAAACAGT AGGGTGAGAC AATCCATTCT CTAAGACCCC TTTAGATCC AAGTCCCCAT AGTTCTGTGG AGTCCCAGTA GAGGCCACCG AGGGTCCCTG GCCCTCTGG GCACAGAGCT GACACTGAGT CCCTCAGTGG CCCCTGAGT ATACCCCTT AGCCGGAGCC CCTTCCCCAT TCCTACAGCC AGAGGGGAC CTGGCCTCAG CCTGGCAGGG CCTCTCTCCT CTTCAAGGCC ATATCCACCT GTGCCCGGG GCTTGGGAGA CCCCTAGGG CCGGAGCTCT GGGGTCACTCC TGGCCACTGG CTTCTCCTT CTCTGTTTG TTCTGTATGT GTTGTGGGGT GGGGGGAGGG GGGCCACCTG CCTTACCTAT TCTGAGTTGC CTTAGAGAG ATGCCTTTT TCTAGGACTC TGTGCAACTG TTGTATATGG TTCCGTGGGC TGACCGCTTT GTACATGAGA ATAATCTAT TTCTTCTAC C	3020 3080 3140 3200 3260 3320 3380 3440 3500 3560 3620 3680 3740 3800 3860 3920 3980 4040 4100 4131

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Arg Gln Pro Ala Ala Ser Arg Asp Leu Phe Ala Gln Glu Pro 1 5 10 15
Val Pro Pro Gly Ser Gly Asp Gly Ala Leu Gln Asp Ala Leu Leu Ser 20 25 30
Leu Gly Ser Val Ile Asp Val Ala Gly Leu Gln Gln Ala Val Lys Glu 35 40 45
Ala Leu Ser Ala Val Leu Pro Lys Val Glu Thr Val Tyr Thr Tyr Leu 50 55 60

Leu Asp Gly Glu Ser Arg Leu Val Cys Glu Glu Pro Pro His Glu Leu
65 70 75 80

Pro Gln Glu Gly Lys Val Arg Glu Ala Val Ile Ser Arg Lys Arg Leu
85 90 95

Gly Cys Asn Gly Leu Gly Pro Ser Asp Leu Pro Gly Lys Pro Leu Ala
100 105 110

Arg Leu Val Ala Pro Leu Ala Pro Asp Thr Gln Val Leu Val Ile Pro
115 120 125

Leu Val Asp Lys Glu Ala Gly Ala Val Ala Val Ile Leu Val His
130 135 140

Cys Gly Gin Leu Ser Asp Asn Glu Glu Trp Ser Leu Gln Ala Val Glu
145 150 155 160

Lys His Thr Leu Val Ala Leu Lys Arg Val Gln Ala Leu Gln Gln Arg
165 170 175

Glu Ser Ser Val Ala Pro Glu Ala Thr Gln Asn Pro Pro Glu Glu Ala
180 185 190

Ala Gly Asp Gln Lys Gly Val Ala Tyr Thr Asn Gln Asp Arg Lys
195 200 205

Ile Leu Gln Leu Cys Gly Glu Leu Tyr Asp Leu Asp Ala Ser Ser Leu
210 215 220

Gln Leu Lys Val Leu Gln Tyr Leu Gln Gln Glu Thr Gln Ala Ser Arg
225 230 235 240

Cys Cys Leu Leu Val Ser Glu Asp Asn Leu Gln Leu Ser Cys Lys
245 250 255

Val Ile Gly Asp Lys Val Leu Glu Glu Ile Ser Phe Pro Leu Thr
260 265 270

Thr Gly Arg Leu Gly Gln Val Val Glu Asp Lys Lys Ser Ile Gln Leu
275 280 285

Lys Asp Leu Thr Ser Glu Asp Met Gln Gln Leu Gln Ser Met Leu Gly
290 295 300

Cys Glu Val Gln Ala Met Leu Cys Val Pro Val Ile Ser Arg Ala Thr
305 310 315 320

Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn Lys Leu Gly Gly Asp
325 330 335

Leu Phe Thr Asp Gln Asp Glu His Val Ile Gln His Cys Phe His Tyr
340 345 350

Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe Gln Lys Glu Gln Lys
355 360 365

Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val Ala Lys Asn Leu Phe
370 375 380

Thr His Leu Asp Asp Val Ser Val Leu Leu Gln Glu Ile Ile Thr Glu
385 390 395 400

Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser Val Phe Leu Leu Asp
405 410 415

Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly Gly Val Val Glu Asp
420 425 430

Glu Ser Tyr Glu Ile Arg Il Pro Ala Asp Gln Gly Ile Ala Gly His
435 440 445

Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro Asp Ala Tyr Ala His
450 455 460

Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr Gly Phe Arg Thr Arg
465 470 475 480

Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn Gln Glu Val Ile Gly
485 490 495

Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro Trp Phe Ser Lys Phe
500 505 510

Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr Cys Gly Ile Ser Ile
515 520 525

Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu Ala Gln Tyr Arg Ser
530 535 540

His Leu Ala Asn Glu Met Met Met Tyr His Met Lys Val Ser Asp Asp
545 550 555 560

Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln Pro Val Ala Ala Ile
565 570 575

Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro Arg Ser Leu Pro Glu
580 585 590

Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu Gln Asp Met Asn Phe
595 600 605

Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu Ala Arg Phe Cys Leu
610 615 620

Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr His Asn Trp Met His
625 630 635 640

Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu Tyr Lys Asn Leu Glu
645 650 655

Leu Thr Asn Tyr Leu Glu Asp Met Glu Ile Phe Ala Leu Phe Ile Ser
660 665 670

Cys Met Cys His Asp Leu Asp His Arg Gly Thr Asn Asn Ser Phe Gln
675 680 685

Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr Ser Ser Glu Gly Ser
690 695 700

Val Met Glu Arg His His Phe Ala Gln Ala Ile Ala Ile Leu Asn Thr
705 710 715 720

His Gly Cys Asn Ile Phe Asp His Phe Ser Arg Lys Asp Tyr Gln Arg
725 730 735

Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala Thr Asp Leu Ala His
740 745 750

His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met Ala Glu Val Gly Tyr
755 760 765

Asp Arg Thr Asn Lys Gln His His Ser Leu Leu Leu Cys Leu L u M t
770 775 780

Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly Trp Lys Thr Thr Arg
785 790 795 800

Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe Ser Gln Gly Asp Leu
805 810 815

Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met Met Asp Arg Glu Lys
820 825 830

Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met Glu His Ile Ala Met
835 840 845

Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro Lys Ala Ala Glu Leu
850 855 860

Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp Thr Lys Val Ser His
865 870 875 880

Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn Ser Leu Asp Phe Leu
885 890 895

Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly Ala Arg Ala Pro Ile
900 905 910

Asn Gly Cys Cys Ser Leu Asp Ala Glu
915 920

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATATCGAATT CGGTTTAGTC TGGTTGCGGA GGCAGACGAT GAGGAGCGAT GGGGCAGGCA 60
TCCGGCCACT CCATCCTCTG CAGGAGCCAG CAGTACCCGG CTGCGCGACC GGCTGAGCCG 120
CGGGGCCAGC AGGTCTTCCT CAAGCCGGAC GAGCCGCCGC CGCCGCCGCA GCCATGCGCC 180
GACAGCCTGC AGGATGCTTT GCTGAGCCTG GGCTCCGTCA TTGAGCTTGC AGGCTTGCAG 240
CAGGCTGTC 249

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTGGGT AGAGCAGGTA GCAGAAGTGG GAGACAGAAA AGGCAGTCAT CCAGTTGTGG 60
TAGGGGGAT CCCGGTAGCC CTTCTTCACC ATCAAACAGA ACCGGGCCAG TGTCGGGCAG 120
TCAATTTGT AGTTATTGAT GAAATTCATG TTCTGCAGCA TGCTCAGGAT GGCCATGGAG 180
TGTCACTCCTT GGGCAGAGAG CGAGGAGTGT ATGTGAACTG GCAAGTTGGA GTCGATGGCA 240
GCCACAGGCT 250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3789 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 181..3006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCGGGAAC TG CCAGGCAGC AGGGCTGGAT TGGGGTGTG AGTCCAGGCT GAGTCGGGA 60
CAGGCCACTG TTCTGGTCC CCGTGCCTGC TGGGCCAGGC GCCCTGCCTG GAGCCCCGGG 120
CAGGGTGGAC AGGGTGAGGT GCCACTTTAG TCTGGTTGGG GAGGCAGACG ATGAGGAGCG 180
ATG GGG CAG GCA TGC GGC CAC TCC ATC CTC TGC AGG AGC CAG CAG TAC 228
Met Gly Gln Ala Cys Gly His Ser Ile Leu Cys Arg Ser Gln Gln Tyr
1 5 10 15
CCG GCT GCG CGA CCG GCT GAG CCG CGG GGC CAG CAG GTC TTC CTC AAG 276
Pro Ala Ala Arg Pro Ala Glu Pro Arg Gly Gln Gln Val Phe Leu Lys
20 25 30
CCG GAC GAG CCG CCG CCG CCG CAG CCA TGC GCC GAC AGC CTG CAG 324
Pro Asp Glu Pro Pro Pro Pro Gln Pro Cys Ala Asp Ser Leu Gln
35 40 45
GAT GCT TTG CTG AGC CTG GGC TCC GTC ATT GAC GTT GCA GGC TTG CAA 372
Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Val Ala Gly Leu Gln
50 ~ 55 60
CAG GCT GTC AAG GAG GCC CTG TCG GCT GTG CTT CCC AAA GTG GAG ACG 420
Gln Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Lys Val Glu Thr
65 70 75 80
GTC TAC ACC TAC CTG CTG GAT GGG GAA TCC CGG CTG GTG TGT GAG GAG 468
Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Arg Leu Val Cys Glu Glu
85 90 95
CCC CCC CAC GAG CTG CCC CAG GAG GGG AAA GTG CGA GAG GCT GTG ATC 516
Pro Pro His Glu Leu Pro Gln Glu Gly Lys Val Arg Glu Ala Val Ile
100 105 110
TCC CGG AAG CGG CTG GGC TGC AAT GGA CTG GGC CCC TCA GAC CTG CCT 564
Ser Arg Lys Arg Leu Gly Cys Asn Gly Leu Gly Pro Ser Asp Leu Pr
115 120 125

GGG AAG CCC TTG GCA AGG CTG GTG GCT CCA CTG GCT CCT GAC ACC CAA Gly Lys Pro L u Ala Arg Leu Val Ala Pro Leu Ala Pro Asp Thr Gln 130 135 140	612
GTG CTG GTC ATA CCG CTG GTG GAC AAG GAG GCC GGG GCT GTG GCA GCT Val Leu Val Ile Pro Leu Val Asp Lys Glu Ala Gly Ala Val Ala Ala 145 150 155 160	660
GTC ATC TTG GTG CAC TGT GGT CAG CTG AGT GAC AAT GAG GAG TGG AGC Val Ile Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu Glu Trp Ser 165 170 175	708
CTG CAA GCT GTG GAG AAG CAT ACC CTG GTG GCC CTG AAA AGG GTG CAG Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Lys Arg Val Gln 180 185 190	756
GCC TTG CAG CAG CGC GAG TCC AGC GTG GCC CCG GAA GCG ACC CAG AAT Ala Leu Gln Gln Arg Glu Ser Ser Val Ala Pro Glu Ala Thr Gln Asn 195 200 205	804
CCT CCG GAG GAG GCA GCG GGA GAC CAG AAG GGT GGG GTC GCA TAC ACA Pro Pro Glu Glu Ala Ala Gly Asp Gln Lys Gly Gly Val Ala Tyr Thr 210 215 220	852
GAC CAA GAC CGA AAG ATC CTG CAG CTT TGC GGG GAG CTC TAC GAC CTG Asp Gln Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu Tyr Asp Leu 225 230 235 240	900
GAT GCA TCT TCC CTG CAG CTC AAA GTC CTC CAA TAT CTG CAA CAG GAG Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu Gln Gln Glu 245 250 255	948
ACC CAG GCA TCC CGC TGC TGC CTG CTG GTC TCC GAG GAC AAT CTT Thr Gln Ala Ser Arg Cys Cys Leu Leu Val Ser Glu Asp Asn Leu 260 265 270	996
CAG CTC TCC TGC AAG GTC ATT GGA GAT AAA GTA CTG GAG GAA GAG ATC Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Glu Glu Glu Ile 275 280 285	1044
AGC TTT CCG TTG ACC ACA GGA CGC CTG GGC CAA GTG GTG GAA GAC AAG Ser Phe Pro Leu Thr Thr Gly Arg Leu Gly Gln Val Val Glu Asp Lys 290 295 300	1092
AAG TCT ATC CAG CTG AAA GAT CTC ACC TCC GAG GAT ATG CAA CAG CTC Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Met Gln Gln Leu 305 310 315 320	1140
CAA AGC ATG TTG GGC TGT GAG GTG CAG GCC ATG CTC TGT GTC CCT GTC Gln Ser Met Leu Gly Cys Glu Val Gln Ala Met Leu Cys Val Pro Val 325 330 335	1188
ATC AGC CGG GCC ACT GAC CAG GTC GTG GCC CTG GCC TGT GCC TTC AAC Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn 340 345 350	1236
AAG CTC GGA GGA GAC TTG TTC ACA GAC CAG GAC GAG CAC GTG ATC CAG Lys Leu Gly Gly Asp Leu Phe Thr Asp Gln Asp Glu His Val Ile Gln 355 360 365	1284
CAC TGC TTC CAC TAC ACC AGC ACA GTG CTC ACC AGC ACC CTG GCC TTC His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe 370 375 380	1332
CAG AAG GAG CAG AAG CTC AAG TGT GAG TGC CAG GCT CTT CTC CAA GTG Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val 385 390 395 400	1380

GCG AAG AAC CTC TTC ACT CAT CTG GAT GAC GTC TCC GTG CTG CTC CAG Ala Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val Val Leu Leu Gln 405	410	415	1428
GAG ATC ATC ACA GAG GCC AGG AAC CTC AGC AAT GCT GAG ATC TGC TCT Glu Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser 420	425	430	1476
GTG TTC CTG CTG GAT CAG AAC GAG CTG GTG GCC AAG GTG TTC GAT GGG Val Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly 435	440	445	1524
GGT GTG GTG GAA GAT GAG AGC TAT GAG ATC CGC ATT CCC GCT GAC CAG Gly Val Val Glu Asp Glu Ser Tyr Glu Ile Arg Ile Pro Ala Asp Gln 450	455	460	1572
GGC ATC GCG GGT CAT GTG GCG ACC ACC GGC CAG ATC CTA AAC ATC CCA Gly Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro 465	470	475	1620
GAT GCT TAC GCA CAT CCG CTT TTC TAC CGA GGC GTG GAC GAC AGC ACC Asp Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr 485	490	495	1668
GGC TTC CGG ACG CGC AAC ATC CTC TGC TTC CCC ATC AAG AAC GAG AAC Gly Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn 500	505	510	1716
CAG GAG GTC ATC GGT GTG GCC GAG CTG GTG AAC AAG ATC AAT GGA CCA Gln Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro 515	520	525	1764
TGG TTC AGC AAG TTT GAT GAA GAC CTG GCT ACA GCC TTC TCC ATC TAC Trp Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr 530	535	540	1812
TGT GGC ATC AGC ATT GCC CAT TCC CTC CTA TAC AAG AAA GTG AAT GAG Cys Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu 545	550	555	1860
GCG CAG TAT CGC AGC CAC CTT GCC AAT GAG ATG ATG ATG TAC CAC ATG Ala Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met Tyr His Met 565	570	575	1908
AAG GTC TCT GAT GAC GAG TAC ACC AAA CTT CTC CAT GAC GGG ATC CAG Lys Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln 580	585	590	1956
CCT GTG GCT GCC ATC GAC TCC AAC TTT GCC AGT TTC ACA TAC ACT CCT Pro Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro 595	600	605	2004
CGC TCT CTG CCC GAG GAT GAC ACT TCC ATG GCC ATC CTG AGC ATG CTG Arg Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu 610	615	620	2052
CAG GAC ATG AAT TTC ATC AAT AAC TAC AAA ATT GAC TGC CCG ACA CTG Gln Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu 625	630	635	2100
GCC CGG TTC TGT TTG ATG GTG AAG AAG GGC TAC CGG GAT CCC CCC TAC Ala Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr 645	650	655	2148
CAC AAC TCG ATG CAC GCC TTT TCT GTC TCC CAC TTC TGC TAC CTG CTC His Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu 660	665	670	2196

TAC AAG AAC CTG GAG CTC ACC AAC TAC CTC GAG GAC ATG GAG ATC TTT Tyr Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Met Glu Ile Ph 675 680 685	2244
GCC TTG TTT ATT TCC TGC ATG TGT CAC GAC CTG GAC CAC AGA GGC ACA Ala Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg Gly Thr 690 695 700	2292
AAC AAC TCC TTC CAG GTG GCC TCG AAA TCT GTG CTG GCC GCG CTC TAC Asn Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr 705 710 715 720	2340
AGC TCG GAA GGC TCT GTC ATG GAG AGG CAC CAC TTC GCT CAG GCC ATT Ser Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln Ala Ile 725 730 735	2388
GCC ATC CTC AAC ACC CAC GGC TGC AAC ATC TTT GAC CAC TTC TCC CGG Ala Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe Ser Arg 740 745 750	2436
AAG GAT TAT CAG CGC ATG TTG GAC CTG ATG CGG GAC ATC ATC TTG GCC Lys Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala 755 760 765	2484
ACA GAT CTG GCC CAC CAC CTC CGC ATC TTC AAG GAC CTC CAA AAG ATG Thr Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met 770 775 780	2532
GCC GAA GTG GGC TAT GAT CGA ACC AAC AAG CAG CAC CAC AGC CTC CTT Ala Glu Val Gly Tyr Asp Arg Thr Asn Lys Gln His His Ser Leu Leu 785 790 795 800	2580
CTC TGC CTC CTT ATG ACC TCC TGT GAC CTC TCT GAC CAG ACC AAG GGC Leu Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly 805 810 815	2628
TGG AAG ACC ACG AGG AAG ATC GCG GAG CTG ATC TAC AAA GAG TTC TTC Trp Lys Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe 820 825 830	2676
TCC CAG CGA GAC TTG GAG AAG GCC ATG GGC AAC AGG CCG ATG GAG ATG Ser Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met 835 840 845	2724
ATG GAC CGT GAG AAG GCC TAC ATC CCC GAG CTG CAG ATC AGC TTC ATG Met Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met 850 855 860	2772
GAG CAC ATC GCA ATG CCC ATC TAC AAG CTG CTG CAA GAC CTG TTC CCC Glu His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro 865 870 875 880	2820
AAG GCG GCC GAG TTG TAC GAA CGC GTG GCC TCT AAT CGT GAG CAC TGG Lys Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp 885 890 895	2868
ACC AAG GTG TCA CAC AAG TTC ACC ATC CGA GGC CTC CCG AGC AAC AAC Thr Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn 900 905 910	2916
TCG TTG GAC TTC CTG GAC GAG GAG TAT GAG GTG CCT GAC CTG GAT GGC Ser Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly 915 920 925	2964
GCT AGG GCT CCC ATC AAT GGC TGT TGC AGC CTT GAT GCT GAG Ala Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu 930 935 940	3006

TGAGTCCCTC	CTGGGACCCC	TCCCTGTCCA	GGCCTCCTCC	CACAAGCCTC	CACGGGCCTG	3066
GCCGCACGCC	CTGGGACCAAG	AGCCAAGGGT	CCTGGATTCT	AGGCCAGGAC	TTCCCATGTG	3126
ACCCGGGCAG	GGTCTGACCT	TCCCAGGCTC	CAGCTTCTT	GTCTGTATAA	TGGAAGACTT	3186
CAGCCTCACT	GAGACTTGT	CACTTGTCTC	CTGAGAGCAC	AGGGGTAACC	AATGAGCACT	3246
GGACCCCTGCT	CTGCACCTCT	GACCGCATCT	TGGCAAGTCC	CCACCCCTCCA	GGCCACTCCT	3306
TCTCTGAGGC	AGCCGGATGG	TTTCTTCTGG	GCCCCATTCC	TGCCCTACCA	GACCTGTGCC	3366
CTTTCCGTG	GGGGCACCC	CACTGGCTCC	CAGGATCCTC	AGGCAAGAAC	ATGAGACATC	3426
TGAGTGGGCA	AAGGGTGGGT	CTTAGAGACA	GTTATCAGCC	TGGCTGGAGG	ACTAGAAAGTA	3486
GCCATGGGAC	CACCTGTGGC	CCAGAGGACT	GCCTTGTCAC	TTATGGTGGG	GACTGGGACC	3546
TGGGGATATA	AGGGTCCCAG	GAGGACACTG	CCAGGGGGCC	AGTGCAGTGC	TCTGGGAGA	3606
GGGGGCTCAG	GAAGAGAGGA	GGATAAGAAC	AGTGAGAAGG	AAGGATCCCT	GGGTTGGGAG	3666
GCAGGCCAG	CATGGGTCAG	CCATGCTTCC	TCCTGGCTGT	GTGACCCCTGG	GCAAGTCCCT	3726
TCCCCCTCTCT	CGAACACAGT	AGGGTGAGAC	AATCCATTCT	CTAAGACCCC	TTTTAGATCC	3786
AAG						3789

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Gly	Gln	Ala	Cys	Gly	His	Ser	Ile	Leu	Cys	Arg	Ser	Gln	Gln	Tyr
1				5					10					15	
Pro	Ala	Ala	Arg	Pro	Ala	Glu	Pro	Arg	Gly	Gln	Gln	Val	Phe	Leu	Lys
			20					25					30		
Pro	Asp	Glu	Pro	Pro	Pro	Pro	Pro	Gln	Pro	Cys	Ala	Asp	Ser	Leu	Gln
	35							40					45		
Asp	Ala	Leu	Leu	Ser	Leu	Gly	Ser	Val	Ile	Asp	Val	Ala	Gly	Leu	Gln
	50					55					60				
Gln	Ala	Val	Lys	Glu	Ala	Leu	Ser	Ala	Val	Leu	Pro	Lys	Val	Glu	Thr
	65					70				75			80		
Val	Tyr	Thr	Tyr	Leu	Leu	Asp	Gly	Glu	Ser	Arg	Leu	Val	Cys	Glu	Glu
				85				90					95		
Pro	Pro	His	Glu	Leu	Pro	Gln	Glu	Gly	Lys	Val	Arg	Glu	Ala	Val	Ile
				100					105				110		
Ser	Arg	Lys	Arg	Leu	Gly	Cys	Asn	Gly	Leu	Gly	Pro	Ser	Asp	Leu	Pro
	115					120						125			
Gly	Lys	Pro	Leu	Ala	Arg	Leu	Val	Ala	Pro	Leu	Ala	Pro	Asp	Thr	Gln
	130					135						140			

Val Leu Val Ile Pro Leu Val Asp Lys Glu Ala Gly Ala Val Ala Ala
145 150 155 160

Val Il Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu Glu Trp Ser
165 170 175

Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Lys Arg Val Gln
180 185 190

Ala Leu Gln Gln Arg Glu Ser Ser Val Ala Pro Glu Ala Thr Gln Asn
195 200 205

Pro Pro Glu Glu Ala Ala Gly Asp Gln Lys Gly Gly Val Ala Tyr Thr
210 215 220

Asp Gln Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu Tyr Asp Leu
225 230 235 240

Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu Gln Gln Glu
245 250 255

Thr Gln Ala Ser Arg Cys Cys Leu Leu Val Ser Glu Asp Asn Leu
260 265 270

Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Glu Glu Glu Ile
275 280 285

Ser Phe Pro Leu Thr Thr Gly Arg Leu Gly Gln Val Val Glu Asp Lys
290 295 300

Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Met Gln Gln Leu
305 310 315 320

Gln Ser Met Leu Gly Cys Glu Val Gln Ala Met Leu Cys Val Pro Val
325 330 335

Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn
340 345 350

Lys Leu Gly Gly Asp Leu Phe Thr Asp Gln Asp Glu His Val Ile Gln
355 360 365

His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe
370 375 380

Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val
385 390 395 400

Ala Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val Leu Leu Gln
405 410 415

Glu Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser
420 425 430

Val Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly
435 440 445

Gly Val Val Glu Asp Glu Ser Tyr Glu Ile Arg Ile Pro Ala Asp Gln
450 455 460

Gly Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro
465 470 475 480

Asp Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr
485 490 495

Gly Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn
500 505 510

Gln Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro
515 520 525

Trp Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr
530 535 540

Cys Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu
545 550 555 560

Ala Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met Tyr His Met
565 570 575

Lys Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln
580 585 590

Pro Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro
595 600 605

Arg Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu
610 615 620

Gln Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu
625 630 635 640

Ala Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr
645 ~ 650 655

His Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu
660 665 670

Tyr Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Met Glu Ile Phe
675 680 685

Ala Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg Gly Thr
690 695 700

Asn Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr
705 710 715 720

Ser Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln Ala Ile
725 730 735

Ala Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe Ser Arg
740 745 750

Lys Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala
755 760 765

Thr Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met
770 775 780

Ala Glu Val Gly Tyr Asp Arg Thr Asn Lys Gln His His Ser Leu Leu
785 790 795 800

Leu Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly
805 810 815

Trp Lys Thr Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe
820 825 830

Ser Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met
835 840 845

Met Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met
850 855 860

Glu His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro
865 870 875 880

Lys Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp
885 890 895

Thr Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn
900 905 910

Ser Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly
915 920 925

Ala Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu
930 935 940

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12..2834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTCTGAT A ATG GGG CAG GCA TGC GGC CAC TCC ATC CTC TGC AGG AGC 50
Met Gly Gln Ala Cys Gly His Ser Ile Leu Cys Arg Ser
1 5 10

CAG CAG TAC CCG GCA GCG CGA CCG GCT GAG CCG CGG GGC CAG CAG GTC 98
Gln Gln Tyr Pro Ala Ala Arg Pro Ala Glu Pro Arg Gly Gln Gln Val
15 20 25

TTC CTC AAG CCG GAC GAG CCG CCG CCG CCG CAG CCA TGC GCC GAC 146
Phe Leu Lys Pro Asp Glu Pro Pro Pro Pro Gln Pro Cys Ala Asp
30 35 40 45

AGC CTG CAG GAC GCC TTG CTG AGT CTG GGC TCT GTC ATC GAC ATT TCA 194
Ser Leu Gln Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Ile Ser
50 55 60

GCC CTG CAA CGT GCT GTC AAG GAG GCC CTG TCA GCT GTG CTC CCC CGA 242
Gly Leu Gln Arg Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Arg
65 70 75

GTG GAA ACT GTC TAC ACC TAC CTA CTG GAT GGT GAG TCC CAG CTG GTG 290
Val Glu Thr Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Gln Leu Val
80 85 90

TGT GAG GAC CCC CCA CAT GAG CTG CCC CAG GAG GGG AAA GTC CGG GAG 338
Cys Glu Asp Pro Pro His Glu Leu Pro Gln Glu Gly Lys Val Arg Glu
95 100 105

GCT ATC ATC TCC CAG AAG CGG CTG GGC TGC AAT GGG CTG GGC TTC TCA 386
Ala Ile Ile Ser Gln Lys Arg Leu Gly Cys Asn Gly Leu Gly Phe Ser
110 115 120 125

GAC CTG CCA GGG AAG CCC TTG GCC AGG CTG GTG GCT CCA CTG GCT CCT Asp Leu Pro Gly Lys Pro Leu Ala Arg Leu Val Ala Pro Leu Ala Pro	434
130 135 140	
GAT ACC CAA GTG CTG GTC ATG CCG CTA GCG GAC AAG GAG GCT GGG GCC Asp Thr Gln Val Leu Val Met Pro Leu Ala Asp Lys Glu Ala Gly Ala	:32
145 150 155	
GTG GCA GCT GTC ATC TTG GTG CAC TGT GGC CAG CTG AGT GAT AA. GAG Val Ala Ala Val Ile Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu	530
160 165 170	
GAA TGG AGC CTG CAG GCG GTG GAG AAG CAT ACC CTG GTC GCC CTG CGG Glu Trp Ser Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Arg	578
175 180 185	
AGG GTG CAG GTC CTG CAG CAG CGC GGG CCC AGG GAG GCT CCC CGA GCC Arg Val Gln Val Leu Gln Arg Gly Pro Arg Glu Ala Pro Arg Ala	626
190 195 200 205	
GTC CAG AAC CCC CCG GAG GGG ACG GCG GAA GAC CAG AAG GGC GGG GCG Val Gln Asn Pro Pro Glu Gly Thr Ala Glu Asp Gln Lys Gly Gly Ala	674
210 215 220	
GCG TAC ACC GAC CGC GAC CGC AAG ATC CTC CAA CTG TGC GGG GAA CTC Ala Tyr Thr Asp Arg Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu	722
225 230 235	
TAC GAC CTG GAT GCC TCT TCC CTG CAG CTC AAA GTG CTC CAA TAC CTG Tyr Asp Leu Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu	770
240 245 250	
CAG CAG GAG ACC CCG GCA TCC CGC TGC TGC CTC CTG CTG GTG TCG GAG Gln Gln Glu Thr Arg Ala Ser Arg Cys Cys Leu Leu Leu Val Ser Glu	818
255 260 265	
GAC AAT CTC CAG CTT TCT TGC AAG GTC ATC GGA GAC AAA GTG CTC GGG Asp Asn Leu Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Gly	866
270 275 280 285	
GAA GAG GTC AGC TTT CCC TTG ACA GGA TGC CTG GGC CAG GTG GTG GAA Glu Glu Val Ser Phe Pro Leu Thr Gly Cys Leu Gly Gln Val Val Glu	914
290 295 300	
GAC AAG AAG TCC ATC CAG CTG AAG GAC CTC ACC TCC GAG GAT GTA CAA Asp Lys Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Val Gln	962
305 310 315	
CAG CTG CAG AGC ATG TTG GGC TGT GAG CTG CAG GCC ATG CTC TGT GTC Gln Leu Gln Ser Met Leu Gly Cys Glu Leu Gln Ala Met Leu Cys Val	1010
320 325 330	
CCT GTC ATC AGC CGG GCC ACT GAC CAG GTG GTG GCC TTG GCC TGC GCC Pro Val Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala	1058
335 340 345	
TTC AAC AAG CTA GAA GGA GAC TTG TTC ACC GAC GAG GAC GAG CAT GTG Phe Asn Lys Leu Glu Gly Asp Leu Phe Thr Asp Glu Asp Glu His Val	1106
350 355 360 365	
ATC CAG CAC TGC TTC CAC TAC ACC AGC ACC GTG CTC ACC AGC ACC CTG Ile Gln His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu	1154
370 375 380	
GCC TTC CAG AAG GAA CAG AAA CTC AAG TGT GAG TGC CAG GCT CTT CTC Ala Phe Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu	1202
385 390 395	

CAA GTG GCA AAG AAC CTC TTC ACC CAC CTG GAT GAC GTC TCT GTC CTG Gln Val Ala Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val Leu	1250
400 405 410	
CTC CAG GAG ATC ATC ACG GAG GCC AGA AAC CTC AGC AAC GCA GAG ATC Leu Gln Glu Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu Ile	1298
415 420 425	
TGC TCT GTG TTC CTG CTG GAT CAG AAT GAG CTG GTG GCC AAG GTG TTC Cys Ser Val Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val Phe	1346
430 435 440 445	
GAC GGG GGC GTG GTG GAT GAT GAG AGC TAT GAG ATC CGC ATC CCG GCC Asp Gly Gly Val Val Asp Asp Glu Ser Tyr Glu Ile Arg Ile Pro Ala	1394
450 455 460	
GAT CAG GGC ATC GCG GGA CAC GTG GCG ACC ACG GGC CAG ATC CTG AAC Asp Gln Gly Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu Asn	1442
465 470 475	
ATC CCT GAC GCA TAT GCC CAT CCG CTT TTC TAC CGC GGC GTG GAC GAC Ile Pro Asp Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp Asp	1490
480 485 490	
AGC ACC GGC TTC CGC ACG CGC AAC ATC CTC TGC TTC CCC ATC AAG AAC Ser Thr Gly Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys Asn	1538
495 500 505	
GAG AAC CAG GAG GTC ATC GGT GTG GCC GAG CTG GTG AAC AAG ATC AAT Glu Asn Gln Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile Asn	1586
510 515 520 525	
GGG CCA TGG TTC AGC AAG TTC GAC GAG GAC CTG GCG ACG GCC TTC TCC Gly Pro Trp Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe Ser	1634
530 535 540	
ATC TAC TGC GGC ATC AGC ATC GCC CAT TCT CTC CTA TAC AAA AAA GTG Ile Tyr Cys Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys Val	1682
545 550 555	
AAT GAG GCT CAG TAT CGC AGC CAC CTG GCC AAT GAG ATG ATG ATG TAC Asn Gl. Ala Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met Tyr	1730
560 565 570	
CAC ATG AAG GTC TCC GAC GAT GAG TAT ACC AAA CTT CTC CAT GAT GGG His Met Lys Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp Gly	1778
575 580 585	
ATC CAG CCT GTG GCT GCC ATT GAC TCC AAT TTT GCA AGT TTC ACC TAT Ile Gln Pro Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr Tyr	1826
590 - 595 600 605	
ACC CCT CGT TCC CTG CCC GAG GAT GAC ACG TCC ATG GCC ATC CTG AGC Thr Pro Arg Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu Ser	1874
610 615 620	
ATG CTG CAG GAC ATG AAT TTC ATC AAC AAC TAC AAA ATT GAC TGC CCG Met Leu Gln Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys Pro	1922
625 630 635	
ACC CTG GCC CGG TTC TGT TTG ATG GTG AAG AAG GGC TAC CGG GAT CCC Thr Leu Ala Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp Pro	1970
640 645 650	
CCC TAC CAC AAC TGG ATG CAC GCC TTT TCT GTC TCC CAC TTC TGC TAC Pro Tyr His Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys Tyr	2018
655 660 665	

CTG CTC TAC AAG AAC CTG GAG CTC ACC AAC TAC CTC GAG GAC ATC GAG Leu Leu Tyr Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Ile Glu 670 675 680 685	2066
ATC TTT GCC TTG TTT ATT TCC TGC ATG TGT CAT GAC CTG GAC CAC AGA Ile Phe Ala Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg 690 695 700	2114
GCG ACA AAC AAC TCT TTC CAG GTG GCC TCG AAA TCT GTG CTG GCT GCG Gly Thr Asn Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala 705 710 715	2162
CTC TAC AGC TCT GAG GGC TCC GTC ATG GAG AGG CAC CAC TTT GCT CAG Leu Tyr Ser Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln 720 725 730	2210
GCC ATC GCC ATC CTC AAC ACC CAC GGC TGC AAC ATC TTT GAT CAT TTC Ala Ile Ala Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe 735 740 745	2258
TCC CGG AAG GAC TAT CAG CGC ATG CTG GAT CTG ATG CGG GAC ATC ATC Ser Arg Lys Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile 750 755 760 765	2306
TTG GCC ACA GAC CTG GCC CAC CAT CTC CGC ATC TTC AAG GAC CTC CAG Leu Ala Thr Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln 770 775 780	2354
AAG ATG GCT GAG GTG GGC TAC GAC CGA AAC AAC AAG CAG CAC CAC AGA Lys Met Ala Glu Val Gly Tyr Asp Arg Asn Asn Lys Gln His His Arg 785 790 795	2402
CTT CTC CTC TGC CTC CTC ATG ACC TCC TGT GAC CTC TCT GAC CAG ACC Leu Leu Leu Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr 800 805 810	2450
AAG GGC TGG AAG ACT ACG AGA AAG ATC GCG GAG CTG ATC TAC AAA GAA Lys Gly Trp Lys Thr Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu 815 820 825	2498
TTC TTC TCC CAG GGA GAC CTG GAG AAG GCC ATG GGC AAC AGG CCG ATG Phe Phe Ser Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met 830 835 840 845	2546
GAG ATG ATG GAC CGG GAG AAG GCC TAT ATC CCT GAG CTG CAA ATC AGC Glu Met Met Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile Ser 850 855 860	2594
TTC ATG GAG CAC ATT GCA ATG CCC ATC TAC AAG CTG TTG CAG GAC CTG Phe Met Glu His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu 865 870 875	2642
TTC CCC AAA GCG GCA GAG CTG TAC GAG CGC GTG GCC TCC AAC CGT GAG Phe Pro Lys Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu 880 885 890	2690
CAC TGG ACC AAG GTG TCC CAC AAG TTC ACC ATC CGC GGC CTC CCA AGT His Trp Thr Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser 895 900 905	2738
AAC AAC TCG CTG GAC TTC CTG GAT GAG GAG TAC GAG GTG CCT GAT CTG Asn Asn Ser Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu 910 915 920 925	2786
GAT GGC ACT AGG GCC CCC ATC AAT GGC TGC TGC AGC CTT GAT GCT GAG Asp Gly Thr Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu 930 935 940	2834

TGACTCGAGC GTCATATTAA TGGACGCCAA GCAAGGAAAT TGCGAGCGGG AAATAAGAAA	2894
CGATAGARGT AGGAATCGAT ACCCGGTGCG TGCACATAAC AGTCTTTAC CAATTAACAG	2954
GAGAGATTGA AGTGTGAGA TACGAAATGA AATTTACTAC GACTACCGTA AACAAATGCA	3014
TAAGCTCTGT TAGAGAAAAA TTGGTAGCCA	3044

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 941 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Gly Gln Ala Cys Gly His Ser Ile Leu Cys Arg Ser Gln Gln Tyr
1 5 10 15

Pro Ala Ala Arg Pro Ala Glu Pro Arg Gly Gln Gln Val Phe Leu Lys
20 25 30

Pro Asp Glu Pro Pro Pro Pro Gln Pro Cys Ala Asp Ser Leu Gln
35 40 45

Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Ile Ser Gly Leu Gln
50 55 60

Arg Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Arg Val Glu Thr
65 70 75 80

Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Gln Leu Val Cys Glu Asp
85 90 95

Pro Pro His Glu Leu Pro Gln Glu Gly Lys Val Arg Glu Ala Ile Ile
100 105 110

Ser Gln Lys Arg Leu Gly Cys Asn Gly Leu Gly Phe Ser Asp Leu Pro
115 120 125

Gly Lys Pro Leu Ala Arg Leu Val Ala Pro Leu Ala Pro Asp Thr Gln
130 135 140

Val Leu Val Met Pro Leu Ala Asp Lys Glu Ala Gly Ala Val Ala Ala
145 150 155 160

Val Ile Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu Glu Trp Ser
165 170 175

Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Arg Arg Val Gln
180 185 190

Val Leu Gln Gln Arg Gly Pro Arg Glu Ala Pro Arg Ala Val Gln Asn
195 200 205

Pro Pro Glu Gly Thr Ala Glu Asp Gln Lys Gly Gly Ala Ala Tyr Thr
210 215 220

Asp Arg Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu Tyr Asp Leu
225 230 235 240

Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu Gln Gln Glu
245 250 255

Thr Arg Ala Ser Arg Cys Cys Leu Leu Leu Val Ser Glu Asp Asn Leu
260 265 270

Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Gly Glu Glu Val
275 280 285

Ser Phe Pro Leu Thr Gly Cys Leu Gly Gln Val Val Glu Asp Lys Lys
290 295 300

Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Val Gln Gln Leu Gln
305 310 315 320

Ser Met Leu Gly Cys Glu Leu Gln Ala Met Leu Cys Val Pro Val Ile
325 330 335

Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn Lys
340 345 350

Leu Glu Gly Asp Leu Phe Thr Asp Glu Asp Glu His Val Ile Gln His
355 360 365

Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe Gln
370 375 380

Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val Ala
385 390 395 400

Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val Leu Leu Gln Glu
405 410 415

Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser Val
420 425 430

Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly Gly
435 440 445

Val Val Asp Asp Glu Ser Tyr Glu Ile Arg Ile Pro Ala Asp Gln Gly
450 455 460

Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro Asp
465 470 475 480

Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr Gly
485 490 495

Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn Gln
500 505 510

Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro Trp
515 520 525

Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr Cys
530 535 540

Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu Ala
545 550 555 560

Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met Tyr His Met Lys
565 570 575

Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln Pro
580 585 590

Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro Arg
595 600 605

Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu Gln
610 615 620

Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu Ala
625 630 635 640

Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr His
645 650 655

Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu Tyr
660 665 670

Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Ile Glu Ile Phe Ala
675 680 685

Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg Gly Thr Asn
690 695 700

Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr Ser
705 710 715 720

Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln Ala Ile Ala
725 730 735

Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe Ser Arg Lys
740 745 750

Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala Thr
755 760 765

Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met Ala
770 775 780

Glu Val Gly Tyr Asp Arg Asn Asn Lys Gln His His Arg Leu Leu Leu
785 790 795 800

Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly Trp
805 810 815

Lys Thr Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe Ser
820 825 830

Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met Met
835 840 845

Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met Glu
850 855 860

His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro Lys
865 870 875 880

Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp Thr
885 890 895

Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn Ser
900 905 910

Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly Thr
915 920 925

Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu
930 935 940

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCRTTNGTNG TNCCYTTCAT RTT

23

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asn Met Lys Gly Thr Thr Asn Asp
1 5

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12..1616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCTGAT C ATG GGG TCT AGT GCC ACA GAG ATT GAA GAA TTG GAA AAC
Met Gly Ser Ser Ala Thr Glu Ile Glu Glu Leu Glu Asn
1 5 10

50

ACC ACT TTT AAG TAT CTT ACA GGA GAA CAG ACT GAA AAA ATG TCG CAG
Thr Thr Phe Lys Tyr Leu Thr Gly Glu Gln Thr Glu Lys Met Trp Gln
15 20 25

98

CGC CTG AAA GGA ATA CTA AGA TGC TTG GTG AAG CAG CTG GAA AGA GGT
Arg Leu Lys Gly Ile Leu Arg Cys Leu Val Lys Gln Leu Glu Arg Gly
30 35 40 45

146

GAT GTT AAC GTC GTC GAC TTA AAG AAG AAT ATT GAA TAT GCG GCA TCT
Asp Val Asn Val Val Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala Ser
50 55 60

194

GTG CTG GAA GCA GTT TAT ATC GAT GAA ACA AGA AGA CTT CTG GAT ACT	242
Val Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp Thr	
65 70 75	
GAA GAT GAG CTC AGT GAC ATT CAG ACT GAC TCA GTC CCA TCT GAA GTC	290
Glu Asp Glu Leu Ser Asp Ile Gln Thr Asp Ser Val Pro Ser Glu Val	
80 85 90	
CGG GAC TGG TTG GCT TCT ACC TTT ACA CGG AAA ATG GGG ATG ACA AAA	338
Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Thr Lys	
95 100 105	
AAG AAA CCT GAG GAA AAA CCA AAA TTT CGG AGC ATT GTG CAT CCT GTT	386
Lys Lys Pro Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val	
110 115 120 125	
CAA GCT GGA ATT TTT GTG GAA AGA ATG TAC CGA AAA ACA TAT CAT ATG	434
Gln Ala Gly Ile Phe Val Glu Arg Met Tyr Arg Lys Thr Tyr His Met	
130 135 140	
GTT GGT TTG GCA TAT CCA GCA GCT GTC ATC GTA ACA TTA AAG GAT GTT	482
Val Gly Leu Ala Tyr Pro Ala Ala Val Ile Val Thr Leu Lys Asp Val	
145 150 155	
GAT AAA TGG TCT TTC GAT GTA TTT GCC CTA AAT GAA GCA AGT GGA GAG	530
Asp Lys Trp Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly Glu	
160 165 170	
CAT AGT CTG AAG TTT ATG ATT TAT GAA CTG TTT ACC AGA TAT GAT CTT	578
His Ser Leu Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp Leu	
175 180 185	
ATC AAC CGT TTC AAG ATT CCT GTT TCT TGC CTA ATC ACC TTT GCA GAA	626
Ile Asn Arg Phe Lys Ile Pro Val Ser Cys Leu Ile Thr Phe Ala Glu	
190 195 200 205	
GCT TTA GAA GTT GGT TAC AGC AAG TAC AAA AAT CCA TAT CAC AAT TTG	674
Ala Leu Glu Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn Leu	
210 215 220	
ATT CAT GCA GCT GAT GTC ACT CAA ACT GTG CAT TAC ATA ATG CTT CAT	722
Ile His Ala Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu His	
225 230 235	
ACA GGT ATC ATG CAC TGG CTC ACT GAA CTG GAA ATT TTA GCA ATG GTC	770
Thr Gly Ile Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met Val	
240 245 250	
TTT GCT GCT GCC ATT CAT GAT TAT GAG CAT ACA GGG ACA ACA AAC AAC	818
Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Asn	
255 - 260 265	
TTT CAC ATT CAG ACA AGG TCA GAT GTT GCC ATT TTG TAT AAT GAT CGC	866
Phe His Ile Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg	
270 275 280 285	
TCT GTC CTT GAG AAT CAC CAC GTG AGT GCA GCT TAT CGA CTT ATG CAA	914
Ser Val Leu Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln	
290 295 300	
GAA GAA GAA ATG AAT ATC TTG ATA AAT TTA TCC AAA GAT GAC TGG AGG	962
Glu Glu Glu Met Asn Ile Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg	
305 310 315	
GAT CTT CGG AAC CTA GTG ATT GAA ATG GTT TTA TCT ACA GAC ATG TCA	1010
Asp Leu Arg Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser	
320 325 330	

GGT CAC TTC CAG CAA ATT AAA AAT ATA AGA AAC AGT TTG CAG CAG CCT Gly His Phe Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro	1058
335 340 345	
GAA CGG ATT GAC AGA GCC AAA ACC ATG TCC CTG ATT CTC CAC GCA GCA Glu Gly Ile Asp Arg Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala	1106
350 355 360 365	
GAC ATC AGC CAC CCA GCC AAA TCC TGG AAG CTG CAT TAT CGG TGG ACC Asp Ile Ser His Pro Ala Lys Ser Trp Lys Leu His Tyr Arg Trp Thr	1154
370 375 380	
ATG GCC CTA ATG GAG GAG TTT TTC CTG CAG GGA GAT AAA GAA GCT GAA Met Ala Leu Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu	1202
385 390 395	
TTA GGG CTT CCA TTT TCC CCA CTT TGT GAT CGG AAG TCA ACC ATG GTG Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val	1250
400 405 410	
GCC CAG TCA CAA ATA GGT TTC ATC GAT TTC ATA GTA GAG CCA ACA TTT Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe	1298
415 420 425	
TCT CTT CTG ACA GAC TCA ACA GAG AAA ATT GTT ATT CCT CTT ATA GAG Ser Leu Leu Thr Asp Ser Thr Glu Lys Ile Val Ile Pro Leu Ile Glu	1346
430 435 440 445	
GAA GCC TCA AAA GCC GAA ACT TCT TCC TAT GTG GCA AGC AGC TCA ACC Glu Ala Ser Lys Ala Glu Thr Ser Ser Tyr Val Ala Ser Ser Ser Thr	1394
450 455 460	
ACC ATT GTG GGG TTA CAC ATT GCT GAT GCA CTA AGA CGA TCA AAT ACA Thr Ile Val Gly Leu His Ile Ala Asp Ala Leu Arg Arg Ser Asn Thr	1442
465 470 475	
AAA GGC TCC ATG AGT GAT GGG TCC TAT TCC CCA GAC TAC TCC CTT GCA Lys Gly Ser Met Ser Asp Gly Ser Tyr Ser Pro Asp Tyr Ser Leu Ala	1490
480 485 490	
GCA GTG GAC CTG AAG AGT TTC AAG AAC AAC CTG GTG GAC ATC ATT CAG Ala Val Asp Leu Lys Ser Phe Lys Asn Asn Leu Val Asp Ile Ile Gln	1538
495 500 505	
CAG AAC AAA GAG AGG TGG AAA GAG TTA GCT GCA CAA GAA GCA AGA ACC Gln Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Glu Ala Arg Thr	1586
510 515 520 525	
AGT TCA CAG AAG TGT GAG TTT ATT CAT CAG TAACTCGAG	1625
Ser Ser Gln Lys Cys Glu Phe Ile His Gln	
530 535	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Ser Ser Ala Thr Glu Ile Glu Glu Leu Glu Asn Thr Thr Phe
1 5 10 15

Lys Tyr Leu Thr Gly Glu Gln Thr Glu Lys Met Trp Gln Arg Leu Lys
20 25 30

Gly Ile Leu Arg Cys Leu Val Lys Gln Leu Glu Arg Gly Asp Val Asn
35 40 45

Val Val Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala Ser Val Leu Glu
50 55 60

Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp Thr Glu Asp Glu
65 70 75 80

Leu Ser Asp Ile Gln Thr Asp Ser Val Pro Ser Glu Val Arg Asp Trp
85 90 95

Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Thr Lys Lys Pro
100 105 110

Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala Gly
115 120 125

Ile Phe Val Glu Arg Met Tyr Arg Lys Thr Tyr His Met Val Gly Leu
130 135 140

Ala Tyr Pro Ala Ala Val Ile Val Thr Leu Lys Asp Val Asp Lys Trp
145 150 155 160

Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly Glu His Ser Leu
165 170 175

Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp Leu Ile Asn Arg
180 185 190

Phe Lys Ile Pro Val Ser Cys Leu Ile Thr Phe Ala Glu Ala Leu Glu
195 200 205

Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn Leu Ile His Ala
210 215 220

Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu His Thr Gly Ile
225 230 235 240

Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met Val Phe Ala Ala
245 250 255

Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Asn Phe His Ile
260 265 270

Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu
275 280 285

Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu
290 295 300

Met Asn Ile Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg
305 310 315 320

Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser Gly His Phe
325 330 335

Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Ile
340 345 350

Asp Arg Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser
355 360 365

His Pro Ala Lys Ser Trp Lys Leu His Tyr Arg Trp Thr Met Ala Leu
370 375 380

Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
385 390 395 400

Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser
405 410 415

Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu
420 425 430

Thr Asp Ser Thr Glu Lys Ile Val Ile Pro Leu Ile Glu Glu Ala Ser
435 440 445

Lys Ala Glu Thr Ser Ser Tyr Val Ala Ser Ser Ser Thr Thr Ile Val
450 455 460

Gly Leu His Ile Ala Asp Ala Leu Arg Arg Ser Asn Thr Lys Gly Ser
465 470 475 480

Met Ser Asp Gly Ser Tyr Ser Pro Asp Tyr Ser Leu Ala Ala Val Asp
485 490 495

Leu Lys Ser Phe Lys Asn Asn Leu Val Asp Ile Ile Gln Gln Asn Lys
500 505 510

Glu Arg Trp Lys Glu Leu Ala Ala Gln Glu Ala Arg Thr Ser Ser Gln
515 520 525

Lys Cys Glu Phe Ile His Gln " "
530 535

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 176..2077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTGCGTTCAA TATTCAAAA TGGATCCGGT TCTGTGGCGG GTGCCAGAGT GAGGCTGTGC 60
GGGACCTCCA GGCGAACCT CCCGAAAGCC TCGGCCTCT CGGTGCCCTG GCCCGGGAG 120
GATAAGGATT TCCCTTCCCT CCTACTTGCG CGCGGAGCCG AGCTCTTGTGTT GAGCT ATG 178
Met 1
GAG TCG CCA ACC AAG GAG ATT GAA GAA TTT GAG AGC AAC TCT CTG AAA 226
Glu Ser Pro Thr Lys Glu Ile Glu Glu Phe Glu Ser Asn Ser Leu Lys
5 10 15
TAC CTG CAA CCG GAA CAG ATC GAG AAA ATC TGG CTT CGG CTC CGC GGG 274
Tyr Leu Gln Pro Glu Gln Ile Glu Lys Ile Trp Leu Arg Leu Arg Gly
20 25 30

CTG AGG AAA TAT AAG AAA ACG TCC CAG AGA TTA CGG TCT TTG GTC AAA Leu Arg Lys Tyr Lys Lys Thr Ser Gln Arg Leu Arg Ser Leu Val Lys 35 40 45	322
CAA TTA GAG AGA GGG GAA GCT TCA GTG GTA GAT CTT AAG AAG AAT TTG Gln Leu Glu Arg Gly Glu Ala Ser Val Val Asp Leu Lys Lys Asn Leu 50 55 60 65	370
GAA TAT GCA GCC ACA GTG CTT GAA TCT GTG TAT ATT GAT GAA ACA AGG Glu Tyr Ala Ala Thr Val Leu Glu Ser Val Tyr Ile Asp Glu Thr Arg 70 75 80	418
AGA CTC CTG GAT ACA GAG GAT GAG CTC AGT GAC ATT CAG TCA GAT GCT Arg Leu Leu Asp Thr Glu Asp Glu Leu Ser Asp Ile Gln Ser Asp Ala 85 90 95	466
GTG CCT TCT GAG GTC CGA GAC TGG CTG GCC TCC ACC TTC ACG CGG CAG Val Pro Ser Glu Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg Gln 100 105 110	514
ATG GGG ATG ATG CTC AGG AGG AGC GAC GAG AAG CCC CGG TTC AAG AGC Met Gly Met Met Leu Arg Arg Ser Asp Glu Lys Pro Arg Phe Lys Ser 115 120 125	562
ATC GTT CAC GCA GTG CAG GCT GGG ATA TTT GTG GAG AGA ATG TAT AGA Ile Val His Ala Val Gln Ala Gly Ile Phe Val Glu Arg Met Tyr Arg 130 135 140 145	610
CGG ACA TCA AAC ATG GTT GGA CTG AGC TAT CCA CCA GCT GTT ATT GAG Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile Glu 150 155 160	658
GCA TTA AAG GAT GTG GAC AAG TGG TCC TTT GAC GTC TTT TCC CTC AAT Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu Asn 165 170 175	706
GAG GCC AGT GGG GAT CAT GCA CTG AAA TTT ATT TTC TAT GAA CTA CTC Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu Leu 180 185 190	754
ACA CGT TAT GAT CTG ATC AGC CGT TTC AAG ATC CCC ATT TCT GCA CTT Thr Arg Tyr Asp Leu Ile Ser Arg Phe Lys Ile Pro Ile Ser Ala Leu 195 200 205	802
GTC TCA TTT GTG GAG GCC CTG GAA GTG GGA TAC AGC AAG CAC AAA AAT Val Ser Phe Val Glu Ala Leu Glu Val Gly Tyr Ser Lys His Lys Asn 210 215 220 225	850
CCT TAC CAT AAC TTA ATG CAC GCT GCC GAT GTT ACA CAG ACA GTG CAT Pro Tyr His Asn Leu Met His Ala Ala Asp Val Thr Gln Thr Val His 230 235 240	898
TAC CTC CTC TAT AAG ACA GGA GTG GCG AAC TGG CTG ACG GAG CTG GAG Tyr Leu Leu Tyr Lys Thr Gly Val Ala Asn Trp Leu Thr Glu Leu Glu 245 250 255	946
ATC TTT GCT ATA ATC TTC TCA GCT GCC ATC CAT GAC TAC GAG CAT ACC Ile Phe Ala Ile Ile Phe Ser Ala Ala Ile His Asp Tyr Glu His Thr 260 265 270	994
GGA ACC ACC AAC AAT TTC CAC ATT CAG ACT CGG TCT GAT CCA GCT ATT Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp Pro Ala Ile 275 280 285	1042
CTG TAT AAT GAC AGA TCT GTA CTG GAG AAT CAC CAT TTA AGT GCA GCT Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Leu Ser Ala Ala 290 295 300 305	1090

TAT CGC CTT CTG CAA GAT GAC GAG GAA ATG AAT ATT TTG ATT AAC CTC Tyr Arg Leu Leu Gln Asp Asp Glu Glu Met Asn Ile Leu Ile Asn Leu 310 315 320	1138
TCA AAG GAT GAC TGG AGG GAG TTT CGA ACC TTG GTA ATT GAA ATG GTG Ser Lys Asp Asp Trp Arg Glu Phe Arg Thr Leu Val Ile Glu Met Val 325 330 335	1186
ATG GCC ACA GAT ATG TCT TGT CAC TTC CAA CAA ATC AAA GCA ATG AAG Met Ala Thr Asp Met Ser Cys His Phe Gln Gln Ile Lys Ala Met Lys 340 345 350	1234
ACT GCT CTG CAG CAG CCA GAA GCC ATT GAA AAG CCA AAA GCC TTA TCC Thr Ala Leu Gln Gln Pro Glu Ala Ile Glu Lys Pro Lys Ala Leu Ser 355 360 365	1282
CTT ATG CTG CAT ACA GCA GAT ATT AGC CAT CCA GCA AAA GCA TCG GAC Leu Met Leu His Thr Ala Asp Ile Ser His Pro Ala Lys Ala Trp Asp 370 375 380 385	1330
CTC CAT CAT CGC TGG ACA ATG TCA CTC CTG GAG GAG TTC TTC AGA CAG Leu His His Arg Trp Thr Met Ser Leu Leu Glu Glu Phe Phe Arg Gln 390 395 400	1378
GGT GAC AGA GAA GCA GAG CTG GGG CTG CCT TTT TCT CCT CTG TGT GAC Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp 405 410 415	1426
CGA AAG TCC ACT ATG GTT GCT CAG TCA CAA GTA GGT TTC ATT GAT TTC Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp Phe 420 425 430	1474
ATC GTG GAA CCC ACC TTC ACT GTG CTT ACG GAC ATG ACC GAG AAG ATT Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys Ile 435 440 445	1522
GTG AGT CCA TTA ATC GAT GAA ACC TCT CAA ACT GGT GGG ACA GGA CAG Val Ser Prc Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly Gln 450 455 460 465	1570
AGG CGT TCG AGT TTG AAT AGC ATC AGC TCG TCA GAT GCC AAG CGA TCA Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Asp Ala Lys Arg Ser 470 475 480	1618
GGT GTC AAG ACC TCT GGT TCA GAG GGA AGT GCC CCG ATC AAC AAT TCT Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn Ser 485 490 495	1666
GTC ATC TCC GTT GAC TAT AAG AGC TTT AAA GCT ACT TGG ACG GAA GTG Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu Val 500 505 510	1714
GTC CAC ATC AAT CGG GAG AGA TGG AGG GCC AAG GTA CCC AAA GAG GAG Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu Glu 515 520 525	1762
AAG GCC AAG AAG GAA GCA GAG GAA AAG GCT CGC CTG GCC GCA GAG GAG Lys Ala Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu Glu 530 535 540 545	1810
CAG CAA AAG GAA ATG GAA GCC AAA AGC CAG GCT GAA GAA GGC GCA TCT Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala Ser 550 555 560	1858
GGC AAA GCT GAG AAA AAG ACG TCT GGA GAA ACT AAG AAT CAA GTC AAT Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val Asn 565 570 575	1906

GGA ACA CGG GCA AAC AAA AGT GAC AAC CCT CGT GGG AAA AAT TCC AAA Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser Lys 580 585 590	1954
GCC GAG AAG TCA TCA GGA GAA CAG CAA CAG AAT GGT GAC TTC AAA GAT Ala Glu Lys Ser Ser Gly Glu Gln Gln Asn Gly Asp Phe Lys Asp 595 600 605	2002
GGT AAA AAT AAG ACA GAC AAG AAG GAT CAC TCT AAC ATC GGA AAT GAT Gly Lys Asn Lys Thr Asp Lys Asp His Ser Asn Ile Gly Asn Asp 610 615 620 625	2050
TCA AAG AAA ACA GAT GAT TCA CAA GAG TAAAAAAGAC CTCATAGACA Ser Lys Lys Thr Asp Asp Ser Gln Glu 630	2097
ATAAAAGAGG CTGCCAGTGT CTTGCATCAT TCTAGCTGAG CTTCTTCATT CTCCTTCTTC TCCTTCTTCC ACAAAAGACCC ATATCTGGAG AAGGTGTACA ACTTCAAAC ACAAGCCCC CACCCCCCTGA CCCTTGGCCT TCCCTCACAC CATCTCCTTC CAGGGGATGA ATCTTGGGG GTTGGTTTGA GGTCTTAGAA CTCTGGGGA TATTCCCTG AGCAAAACAA ACAACGTGAG ATTTTTACTC AAACAGAAC AAAACATGAA GGGGCATCCT CAAAATCCTT TGCTAATGAC CTGGCTTTCA AGGCATCTGT CTGGCCTGAT GAGAATGGAC ATCCTGGATA TGCTGGAGA GGCCTGAAAA AAGCCACACA CACAGTAATT GCCATTTAT GACTGTCAAT GCCGTTACTT TAAATGTTGT CATTGGCA CTGGCTACTG ATGATACAGC CATGCTGACA TTCATCACCG CAAAGATGAT GATTCCAGTC TCTGGTTCCCT TTCCCTGAGTC AGGAACATTT GTTTCTCCA ATTCCTTTC AGACTAAAA TTGTTCTTAT GCTTTTTTC CCACTTCTGT AATACA	2157 2217 2277 2337 2397 2457 2517 2577 2637 2693

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 634 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Ser Pro Thr Lys Glu Ile Glu Glu Phe Glu Ser Asn Ser Leu
1 5 10 15

Lys Tyr Leu Gln Pro Glu Gln Ile Glu Lys Ile Trp Leu Arg Leu Arg
20 25 30

Gly Leu Arg Lys Tyr Lys Lys Thr Ser Gln Arg Leu Arg Ser Leu Val
35 40 45

Lys Gln Leu Glu Arg Gly Glu Ala Ser Val Val Asp Leu Lys Lys Asn
50 55 60

Leu Glu Tyr Ala Ala Thr Val Leu Glu Ser Val Tyr Ile Asp Glu Thr
65 70 75 80

Arg Arg Leu Leu Asp Thr Glu Asp Glu Leu Ser Asp Ile Gln Ser Asp
85 90 95

Ala Val Pro Ser Glu Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg
100 105 110

Gln Met Gly Met Met Leu Arg Arg Ser Asp Glu Lys Pro Arg Phe Lys
115 120 125

Ser Ile Val His Ala Val Gln Ala Gly Ile Phe Val Glu Arg Met Tyr
130 135 140

Arg Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile
145 150 155 160

Glu Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu
165 170 175

Asn Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu
180 185 190

Leu Thr Arg Tyr Asp Leu Ile Ser Arg Phe Lys Ile Pro Ile Ser Ala
195 200 205

Leu Val Ser Phe Val Glu Ala Leu Glu Val Gly Tyr Ser Lys His Lys
210 215 220

Asn Pro Tyr His Asn Leu Met His Ala Ala Asp Val Thr Gln Thr Val
225 230 235 240

His Tyr Leu Leu Tyr Lys Thr Gly Val Ala Asn Trp Leu Thr Glu Leu
245 250 255

Glu Ile Phe Ala Ile Ile Phe Ser Ala Ala Ile His Asp Tyr Glu His
260 265 270

Thr Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp Pro Ala
275 280 285

Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Leu Ser Ala
290 295 300

Ala Tyr Arg Leu Leu Gln Asp Asp Glu Glu Met Asn Ile Leu Ile Asn
305 310 315 320

Leu Ser Lys Asp Asp Trp Arg Glu Phe Arg Thr Leu Val Ile Glu Met
325 330 335

Val Met Ala Thr Asp Met Ser Cys His Phe Gln Gln Ile Lys Ala Met
340 345 350

Lys Thr Ala Leu Gln Gln Pro Glu Ala Ile Glu Lys Pro Lys Ala Leu
355 360 365

Ser Leu Met Leu His Thr Ala Asp Ile Ser His Pro Ala Lys Ala Trp
370 375 380

Asp Leu His His Arg Trp Thr Met Ser Leu Leu Glu Glu Phe Phe Arg
385 390 395 400

Gln Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys
405 410 415

Asp Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp
420 425 430

Phe Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys
435 440 445

Ile Val Ser Pro Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly
450 455 460

Gln Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Ser Asp Ala Lys Arg
465 470 475 480

Ser Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn
485 490 495

Ser Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu
500 505 510

Val Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu
515 520 525

Glu Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu
530 535 540

Glu Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala
545 550 555 560

Ser Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val
565 570 575

Asn Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser
580 585 590

Lys Ala Glu Lys Ser Ser Gly Glu Gln Gln Gln Asn Gly Asp Phe Lys
595 600 605

Asp Gly Lys Asn Lys Thr Asp Lys Asp His Ser Asn Ile Gly Asn
610 615 620

Asp Ser Lys Lys Thr Asp Asp Ser Gln Glu
625 630

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2077 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

A CGG ACA TCA AAC ATG GTT GGA CTG AGC TAT CCA CCA GCT GTT ATT 46
Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile
1 S 10 :5

GAG GCA TTA AAG GAT GTG GAC AAG TGG TCC TTT GAC GTC TTT TCC CTC 94
Glu Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu
20 25 30

AAT GAG GCC AGT GGG GAT CAT GCA CTG AAA TTT ATT TTC TAT GAA CTA 142
Asn Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu
35 40 45

CTC ACA CGT TAT GAT CTG ATC AGC CGT TTC AAG ATC CCC ATT TCT GCA	190
Leu Thr Arg Tyr Asp Leu Ile Ser Arg Phe Lys Ile Pro Ile Ser Ala	
50 55 60	
CTT GTC TCA TTT GTG GAG GCC CTG GAA GTG GGA TAC AGC AAG CAC AAA	238
Leu Val Ser Phe Val Glu Ala Leu Glu Val Gly Tyr Ser Lys His Lys	
65 70 75	
AAT CCT TAC CAT AAC TTA ATG CAC GCT GCC GAT GTT ACA CAG ACA GTG	286
Asn Pro Tyr His Asn Leu Met His Ala Ala Asp Val Thr Gln Thr Val	
80 85 90 95	
CAT TAC CTC CTC TAT AAG ACA GGA GTG GCG AAC TGG CTG ACG GAG CTG	334
His Tyr Leu Leu Tyr Lys Thr Gly Val Ala Asn Trp Leu Thr Glu Leu	
100 105 110	
GAG ATC TTT GCT ATA ATC TTC TCA GCT GCC ATC CAT GAC TAC GAG CAT	382
Glu Ile Phe Ala Ile Ile Phe Ser Ala Ala Ile His Asp Tyr Glu His	
115 120 125	
ACC GGA ACC ACC AAC AAT TTC CAC ATT CAG ACT CGG TCT GAT CCA GCT	430
Thr Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp Pro Ala	
130 135 140	
ATT CTG TAT AAT GAC AGA TCT GTA CTG GAG AAT CAC CAT TTA AGT GCA	478
Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Leu Ser Ala	
145 150 155	
GCT TAT CGC CTT CTG CAA GAT GAC GAG GAA ATG AAT ATT TTG ATT AAC	526
Ala Tyr Arg Leu Leu Gln Asp Asp Glu Glu Met Asn Ile Leu Ile Asn	
160 165 170 175	
CTC TCA AAG GAT GAC TGG AGG GAG TTT CCA ACC TTG GTA ATT GAA ATG	574
Leu Ser Lys Asp Asp Trp Arg Glu Phe Arg Thr Leu Val Ile Glu Met	
180 185 190	
GTG ATG GCC ACA GAT ATG TCT TGT CAC TTC CAA CAA ATC AAA GCA ATG	622
Val Met Ala Thr Asp Met Ser Cys His Phe Gln Gln Ile Lys Ala Met	
195 200 205	
AAG ACT GCT CTG CAG CAG CCA GAA GCC ATT GAA AAG CCA AAA GCC TTA	670
Lys Thr Ala Leu Gln Gln Pro Glu Ala Ile Glu Lys Pro Lys Ala Leu	
210 215 220	
TCC CTT ATG CTG CAT ACA GCA GAT ATT AGC CAT CCA GCA AAA GCA TGG	718
Ser Leu Met Leu His Thr Ala Asp Ile Ser His Pro Ala Lys Ala Trp	
225 230 235	
GAC CTC CAT CAT CGC TGG ACA ATG TCA CTC CTG GAG GAG TTC TTC AGA	766
Asp Leu His His Arg Trp Thr Met Ser Leu Leu Glu Glu Phe Phe Arg	
240 245 250 255	
CAG GGT GAC AGA GAA GCA GAG CTG GGG CTG CCT TTT TCT CCT CTG TGT	814
Gln Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys	
260 265 270	
GAC CGA AAG TCC ACT ATG GTT GCT CAG TCA CAA GTA GGT TTC ATT GAT	862
Asp Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp	
275 280 285	
TTC ATC GTG GAA CCC ACC TTC ACT GTG CTT ACG GAC ATG ACC GAG AAG	910
Phe Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys	
290 295 300	
ATT GTG AGT CCA TTA ATC GAT GAA ACC TCT CAA ACT GGT GGG ACA GGA	958
Ile Val Ser Pro Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly	
305 310 315	

CAG AGG CGT TCG ACT TTG AAT AGC ATC AGC TCG TCA GAT GCC AAG CGA 320	Gln Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Ser Asp Ala Lys Arg 325	330	335	1006
TCA GGT GTC AAG ACC TCT GGT TCA GAG GGA AGT GCC CCG ATC AAC AAT Ser Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn 340	345	350		1054
TCT GTC ATC TCC GTT GAC TAT AAG AGC TTT AAA GCT ACT TGG ACG GAA Ser Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu 355	360	365		1102
GTG GTG CAC ATC AAT CGG GAG AGA TGG AGG GCC AAG GTA CCC AAA GAG Val Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu 370	375	380		1150
GAG AAG GCC AAG AAG GAA GCA GAG GAA AAG GCT CGC CTG GCC CCA GAG Glu Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu 385	390	395		1198
GAG CAG CAA AAG GAA ATG GAA GCC AAA AGC CAG GCT GAA GAA GGC GCA Glu Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala 400	405	410	415	1246
TCT GGC AAA GCT GAG AAA AAG ACG TCT GGA GAA ACT AAG AAT CAA GTC Ser Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val 420	425	430		1294
AAT GGA ACA CGG GCA AAC AAA AGT GAC AAC CCT CGT GGG AAA AAT TCC Asn Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser 435	~ 440	445		1342
AAA GCT GAG AAG TCA TCA GGA GAA CAG CAA CAG AAT GGT GAC TTC AAA Lys Ala Glu Lys Ser Ser Gly Glu Gln Gln Asn Gly Asp Phe Lys 450	455	460		1390
GAT GGT AAA AAT AAG ACA GAC AAG AAG GAT CAC TCT AAC ATC GGA AAT Asp Gly Lys Asn Lys Thr Asp Lys Asp His Ser Asn Ile Gly Asn 465	470	475		1438
GAT TCA AAG AAA ACA GAT GGC ACA AAA CAG CGT TCT CAC GGC TCA CCA Asp Ser Lys Lys Thr Asp Gly Thr Lys Gln Arg Ser His Gly Ser Pro 480	485	490	495	1486
GCC CCA AGC ACC AGC TCC ACG TGT CGC CTT ACG TTG CCA GTC ATC AAG Ala Pro Ser Thr Ser Ser Thr Cys Arg Leu Thr Leu Pro Val Ile Lys 500	505	510		1534
CCT CCT TTG CGT CAT TTT AAA CGC CCT GCT TAC GCA TCT AGC TCC TAT Pro Pro Leu Arg His Phe Lys Arg Pro Ala Tyr Ala Ser Ser Ser Tyr 515	520	525		1582
GCA CCT TCA GTC TCA AAG AAA ACT GAT GAG CAT CCT GCA AGG TAC AAG Ala Pro Ser Val Ser Lys Lys Thr Asp Glu His Pro Ala Arg Tyr Lys 530	535	540		1630
ATG CTA GAT CAG AGG ATC AAA ATG AAA AAG ATT CAG AAC ATC TCA CAT Met Leu Asp Gln Arg Ile Lys Met Lys Lys Ile Gln Asn Ile Ser His 545	550	555		1678
AAC TGG AAC AGA AAA TAGGCCGAGG GGAAGAAGAG AGGGAGTGAA GGAGGGTCTA Asn Trp Asn Arg Lys 560				1733
CCTATCTGCT TCTCAGCACC CACTGGCAC ACGCAGGACAC ACCTCCAAGA CCCTTGGAGG CTGTTGGAGC AGGTACTATC CTGGTTGACT CCACCAAGGT GAAATGAAAG TTGTATGTGA				1793
				1853

TTTCCTCTT TGTTGTTCTT GTATAGACTT TTCAATTGCT GTATGTGGGA TCAGCCCAGA	1913
CGCCAGCAAC AAACTAGCAA GAGGGGTGTT TTTATGGTAT AAGTCTCTAA AAGTCTAAAT	1973
TGGACCAAAA TTAAAATGAC ACAAACTTAA AAAAAAATAA AATTCCCTCTC ATTGCCACTT	2033
TTTCAATCT CTAAAAGTTA CTTGCCCCCA AAAGAATATT GGTC	2077

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile Glu	
1 5 10 15	
Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu Asn	
20 25 30	
Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu Leu	
35 40 45	
Thr Arg Tyr Asp Leu Ile Ser Arg Phe Lys Ile Pro Ile Ser Ala Leu	
50 55 60	
Val Ser Phe Val Glu Ala Leu Glu Val Gly Tyr Ser Lys His Lys Asn	
65 70 75 80	
Pro Tyr His Asn Leu Met His Ala Ala Asp Val Thr Gln Thr Val His	
85 90 95	
Tyr Leu Leu Tyr Lys Thr Gly Val Ala Asn Trp Leu Thr Glu Leu Glu	
100 105 110	
Ile Phe Ala Ile Ile Phe Ser Ala Ala Ile His Asp Tyr Glu His Thr	
115 120 125	
Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp Pro Ala Ile	
130 135 140	
Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Leu Ser Ala Ala	
145 150 155 160	
Tyr Arg Leu Leu Gln Asp Asp Glu Glu Met Asn Ile Leu Ile Asn Leu	
165 170 175	
Ser Lys Asp Asp Trp Arg Glu Phe Arg Thr Leu Val Ile Glu Met Val	
180 185 190	
Met Ala Thr Asp Met Ser Cys His Phe Gln Gln Ile Lys Ala Met Lys	
195 200 205	
Thr Ala Leu Gln Gln Pro Glu Ala Ile Glu Lys Pro Lys Ala Leu Ser	
210 215 220	
Leu Met Leu His Thr Ala Asp Ile Ser His Pro Ala Lys Ala Trp Asp	
225 230 235 240	
Leu His His Arg Trp Thr Met Ser Leu Leu Glu Glu Phe Phe Arg Gln	
245 250 255	

Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp
260 265 270

Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp Phe
275 280 285

Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys Ile
290 295 300

Val Ser Pro Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly Gln
305 310 315 320

Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Asp Ala Lys Arg Ser
325 330 335

Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn Ser
340 345 350

Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu Val
355 360 365

Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu Glu
370 375 380

Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu Glu
385 390 395 400

Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala Ser
405 410 415

Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val Asn
420 425 430

Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser Lys
435 440 445

Ala Glu Lys Ser Ser Gly Glu Gln Gln Asn Gly Asp Phe Lys Asp
450 455 460

Gly Lys Asn Lys Thr Asp Lys Asp His Ser Asn Ile Gly Asn Asp
465 470 475 480

Ser Lys Lys Thr Asp Gly Thr Lys Gln Arg Ser His Gly Ser Pro Ala
485 490 495

Pro Ser Thr Ser Ser Thr Cys Arg Leu Thr Leu Pro Val Ile Lys Pro
500 505 510

Pro Leu Arg His Phe Lys Arg Pro Ala Tyr Ala Ser Ser Ser Tyr Ala
515 520 525

Pro Ser Val Ser Lys Lys Thr Asp Glu His Pro Ala Arg Tyr Lys Met
530 535 540

Leu Asp Gln Arg Ile Lys Met Lys Lys Ile Gln Asn Ile Ser His Asn
545 550 555 560

Trp Asn Arg Lys

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TACGAAGCTT TGATGGGTC TACTGCTAC

29

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TACGAAGCTT TGATGGTTGG CTTGGCATAT C

31

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATTACCCCTC ATAAAG

16

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TACGAAGCTT TGATGCGCCG ACAGCCTGC

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGTCTCCTGT TGCAGATATT G